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Matches 9; Conservative
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                                                                                                      pathways:
skeletal muscle type : exons 1/3/5-10/11/12
smooth muscle type : exons 1/2/5-10/13
nonmuscle type : exons 4/5-10/7
Data kindly reviewed (18-SEP-1989) by Lindquester G.J.
                                                                                                                                                                                                                                                                                                                                  Erratum:[[published erratum appears in DNA Seq 1993;3(5):337]] see X16230 - X16241 for alpha-tropomyosin gene exons 1-13. splicing
                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Seq. 2 (6), 343-346 (1992)
93075997
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Kristensen,T., Lopez,R. and Prydz,H.
An estimate of the sequencing error frequency in the DNA sequence databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avian tropomyosin gene expression Nucleic Acids Res. 17 (5), 2099-2118 (1989)
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Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
1 (bases 1 to 1972)
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LARVERVIVVSMNYRGGALGFLALFONPEVPGNWGLFDQQLALQWVQKNIAAFGSNPK
SVTLFGSAGAGSVSLHLLSPRSQPLFTRAIIQSGSSKAPWAVMSLDEAKNRTLTLAK
FIGCSKENDFEIIKCLAKKDPQEILLLWELLVVPSDTLLSVNGOPVVDGDELTDMPDTL
LQLGQFKKTQILVGVNKDEGTAFLVYGAPGFSKDNDSIITRKEFQEGLKIYFPGVSEF
GREALLFYYVDLLDDQRAEKYREALDDVLGDYNIICFALEFTYFSELGNNAFFYYFS
HRSSQLPWFEWMGVMIGYEIEFYFGLLDERRWYTRAEEILSRSIMNYWANAFAKYGNE
MGTQNNSTRWBAFRSTDOKYLTLNAESPKYYTKLRAQCCRFWFLFFPKVLEMTGNIDE
AEREWBAFRSTDOKYLTLNAESPKYYTKLRAQCCRFWFLFFPKVLEMTGNIDE
AEREWBAGFYRWNNYMDWKNQFNDYTSKKESCAGL"
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NLPVLDGTVTAFLGIPYAQPPLGRLRFKKPQFLTKWSDIWNATKYANSCYQNADQSFP
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375 c 409 g 550 t
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/protein_id="AACO6361.1"
/db_xref="pri:92981241"
/db_xref="G1:2981241"
/organism="Coturnix coturnix"
/strain="Japanese."
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U80060
g2351572
U80060.1 GI:2351572
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AF084366
g3450894
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Naegleria italica
Naegleria italica
Eukaryotae; mitochondrial eukaryotes; Heterolobosea;
Eukaryotae; witochondrial eukaryotes; Heterolobosea;
Schizopyrenida; Vahlkampfiidae; Naegleria.
1 (bases 1 to 1974)
Einvik,C., Decatur,W.A., Embley,T.M., Vogt,V.M. and Johansen,S.
Naegleria nucleolar introns contain two group I ribozymes with different functions in RNA splicing and processing
                        Lactobacillus cds.
                                                   AF084366
                                                                                                                                                                                                                                                                                                                        Embley,T.M and Dyal,P.L.
Direct Submission
Submitted (27-NOV-1996) Zoology, Natural History Museum, Cromwell
                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Similarity 100.0%;
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/organism="Naegleria italica"
/strain="AB-T-F3"
/db_xref="taxon:36334"
<1. .>1974
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251. 1180
/label=ex13
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/note="putative VECTOR contamination M13mp18"
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/usedin=X16230:trop_cds
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Pred. No. 8.17e+03;
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ribosomal RNA gene, partial
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U09869
Van Bastelaere,E., Keijers,V. and Vanderleyden,J. Cloning and sequencing of the putative Azospirillum brasilense encoding GTP cyclohydrolase II
                                                                                              Azospirillum brasilense
Azospirillum brasilense
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Foran,D.R., Johnson,P.J. and Moore,G.P.
Evolution of two actin genes in the sea urchin Strongylocentrotus
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Strongylocentrotus franciscanus
Eukaryota, Metazoa, Echinodermata; I
Euechinoidea; Echinacea; Echinoida;
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                                                                               Eubacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
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1018. .1876
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1018. .120
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/translation="MCDDVAALVIDNSGMVKAGFAGDDAPRAVFPSIVGRPRHQGV
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ETCYNSIMKCDVDIRKDLYANTVLSGGSTMFFGIADRWQKEITALAPPTMKIKIKIAPP
ETKYSVMIGGSILASLSTFQQMWISKQEYDESGPSIVHRKCF"
                                                                                                                                              GI:497270
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/db_xref="taxon:7665"
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AF053483.1
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Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
Sequence and characterization of domestic cat acetylcholinesterase
and butyrylcholinesterase
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Submitted (20-MAY-1994) Els Van
Laboratory of Genetics, Applied
42, Heverlee, B-3001, Belgium
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95189096
                                                                                                                                       Submitted (11-MAR-1998) Eppley Institute, University of Nebraska Medical Center, 600 S. 42nd St., Omaha, NE 68198-6805, USA Location/Qualifiers
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Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
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                                                                                                                                                                                                                                             Unpublished
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Carnivora; Fissipedia; Felidae; Felis.
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                /gene="BCHE"
89. .172
                                                   /tissue_type="pituitary"
1. .1932
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HTGSAAEWAAEHDLLLVRARDIADYRYHVRTLRVAEARVPLSGAENTSIAAFRPID
GGPEHLAITVGNPVAGEPVLARLHSEGFTGDLLAGLRCDGQOLRGAIAEIAHGSGY
LLYLAQEGRGIGLVNKLRAYRIQDRGFDTVDANEILGFEADERVYLPAAEMLRQLGFT.
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'gene="BCHE"
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1 (bases 1 to 2136)
Latta, M., Mayaux, J.F. and Sarmientos, P.
Method for the synthesis of mature human serum albumin Patent: EP 0236210-A 6 09-SEP-1987;
                                                                       S73803 2
HLC-32=32 kda
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/TIANSLATION-"MPNIKYADGEVVMGRWPGSVLYYEVQVTSYDDASHLYTVKYKDG
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REDKKK I IQETSLAP PK PSENNTRRYNEDEDSTERNDTSSKLLEQQKLKPDVEMEPVL
DQYSLHSRREEKKKEITYAEKKI FEALKTPEKPSSKTNELEFGGREGTFMLMFELPAT
VLYLVLMCKQDDPSLMNFPLPALESLWETKVFGVFLLWFFFQALFYLLPIGKVVEGL
YLYLVLMCKQDDPSLMNFPLALESLWETKVFGVFLLWFFFQALFYLLPIGKVVEGL
YLYLRSLKAPEEDLAPGGNGSTLYVFDFTGHELMPTLYDTWOFEVSAAFENALSI
YLYIRSLKAPEEDLAPGGNGSTLYVFDFTGHELMPTLYFFEVER
NLAMLLAEMKIHNQSMPSLSMILVNSFQLLYVDALMWEESPLKKYFELERGGLIGWVI
NLAMLLAEMKIHNGSMPSLSMILVNSFQLLYFTUALAWSLEGGENHLILFYFFY
DDPKLSYLKVLPTATGKGLLYNGWGFVRHPNYLGGIIMALAWSLPGGENHLILFYFFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="lamin B recepto
/evidence=experimental
103. .2016
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="PID:g62934"
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                                                                                                              Submitted (08-JUN-1998) Duffieux F., Universite B. Pascal-UPESA CNRS 6023, Protistologie Mol. et Cell. des Parasites Opportunistes, Campus des Cezeaux, 24 av. des Landais, Aubiere, 63177, FRANCE 2 (bases 1 to 2157)
Duffieux,F., Peyret,P., Roe,B.A. and Vivares,C.P.
Putative trehalose 6-phosphate phosphatase from the chromosome I of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 156426) from the original journal article. This sequence comes from Fig. 3.

Location/Qualifiers
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Echinoidea
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Brennan, C. and Robinson, J.J.
                                                                         Unpublished
                                                                                                Encephalitozoon cuniculi (Microspora)
                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                        Duffieux,F.
                                                                                                                                                                                                                                                                    Eukaryota; Microsporidia;
1 (bases 1 to 2157)
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                                                                                                                                                                                                                                                                                                                                                      trehalose 6-phosphate phosphatase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphatase.
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLPWCFGSMDPFTRGLGCLKASISAKFSCFSRRSGMSVGVAIAN PMYLSFAKFSCFSRRSGMSVGVAIAN PMYLSFALENOALREAA SAKEFLRKMFPADSMYGSFARSDNRVDEDGRAKKLTVEAWYS GRYESGYDLROYLROSDLSSVTLCMFSDSKAVGKWRFGLLPAKLRPDQEAMKNLVEAWYS GRYESSQISDNQKYQSLINGAKLRFNYYARDSKKMITANGARVVEADRKASSGLIHVVD KYIYPLPVGNYMSTLADNPAFSMYVDLKQAGLEDEVRNSDPITVLVFTNAAFQALPA GYLDDLKKDAFCALPAKKHKIKKHYISDWKYSYSILSSGQRARASGGDEISVARDSDQILL NKQSDQSKASRVILRDIPTTNGYIQVIDRVILPSQKHFVLV"
/organism="Encephalitozoon cuniculi"
/isolate="mouse"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAB32327.1"
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/db_xref="taxon:7625"
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                                                       ocation/Qualifiers
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Pred. No.
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8.17e+03;
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KEYWORDS
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Best Local Similarity 100.0%;
Matches 9; Conservative
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1 (bases 1 to 2160)

Hansen,A.J. and May B.K.
Sequence of a chicken phenobarbital-inducible cytochrome P450 cDNA:
Regulation of two P450 mRNAs transcribed from different genes
DNA 8, 179-191 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHKCYP450Z 2160 bp mRNA VR1
Chicken phenobarbital-inducible cytochrome
M25469
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M25469.1 GI:532117
Cytochrome P450.
Gallus gallus CDNA to mRNA.
Gallus gallus
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/db_xref="piD:e1316154"

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/db_xref="piD:e1316154"

/db_xref="piD:e1316154"

/db_xref="piD:e1316154"

/db_xref="piD:e1316154"

/db_xref="piD:e1376049"

/db_xref="piD:e1376049"

/db_xref="piD:e13776049"

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                     /organism="Gallus gallus"
/db_xref="taxon:9031"
40. .1515
                            VFQLNPWDLMESFKELSKKYGPIFTIHLGPKKVVVLYGYDVVKEALIDNGEAFSGRGN
LPLFEKFKGTGIVTSNGESMRQMRRFALTTLADFGMGKSIERIGEEARFLVERIR
NTHEKPFNPTVELMHAVSNIIGSTVFGDRFDYEDKKFLDLIEMLDENERFQURIQOR,
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/protein id="AAA48743.1"
/db_xref="FDI:9532118"
/db_xref="GI:532118"
/translation="MDFLGLPTILLLVCISCFLIAAWRSTSQRGKEPPGPTPIIGN
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/protein id="CAA07262.1"
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                                                                                                                                                                                                                                                                                                                                           /note="phenobarbital-inducible"
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/chromosome="I"
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d. No. 8.17e+
Mismatches
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8.17e+03;
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P450 mRNA, complet
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                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local Similarity 100.0%;
Matches 9; Conservative
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ttctgagaa 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-MAY-1992) P. Arcari, Dipartimento di Biotecnologie Mediche, University of Naples, Via S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sulfolobus solfataricus. Sulfolobus solfataricus
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SPILQDCKEFPNEKFDPGHFLMANGTFRKSNYEMPFSAGKRICAGEGLARMELFLFL
TSILQNESLKPVKDRKDIDISPIYTSAANIPRPYEVSFIPR"
2130. . 2135
a 505 c 470 g 566 t
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/db_xref="SWISS-PROT: P39460"
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VRATIYRRAADQKEVKKPEYNSLYVDEALGKKYLRVYSCNTTALLATICTYNMAVIAFTEL
VRATIYRRAADQKEVKKPEINSLYVDEALGKKYLRVYSCNTTALLATICTYNMAVIAFTEL
VRATIYRRAADQKEVKKPEINSLYVDEALGKKYLRVYSCNTALLATICTYNMAVIAFTEL
VRATIYRRAADQKEVKKPEINSLYDDEATVSHAKDVIAFATAELVEVARDLKRDRNDI
MHMHFINITLKDKVEKKDILSVLENTPRIVLISSKYDAEATAELVEVARDLKRDRNDI

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ILKGYLI"
                                                                                                                                                                                                                                                                                                                                                                                                    /product="glyceraldehyde 3-phosphate dehydrogenase"
/protein_id="CAA47040.1"
/db_xref="PID:9809766"
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/strain="MT-4 (ATCC 49255)"
/db_xref="taxon:2287"
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Pred. No.
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                                                                                                       Score 9; DB 17;
Pred. No. 8.17e+03
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CDS.
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                            B.taurus mitochondrial aspartate aminotransferase mRNA, complete
                                             BTASPAMTA
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Lee, M.-H., Shroff, R. and Hope, R.
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Vertebrata; Monotremata; Tachyglossidae; Tachyglossus
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2120. .2170
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/protein_id="AAB42177.1"
/db_xref="PID:g438907"
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/gene="HBB"
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/db_xref-"taxon:9261"
/dev_stage-"adult"
/sex-"female"
                                                                                                                                                                                                                                                                                                                      /gene="HBB"
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/number=2
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FGDLSSADAVMGNAKVKAHGAKVLTSFGDALKNLDNLKGTFAKLSELHCDKLHVDPE
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Z25466.1
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Direct Submission
Officer Palmisano, c/o Dip.
Submitted (15-OCT-1993) Antonietta Palmisano, c/o Dip.
Submitted (15-OCT-1993) Antonietta Palmisano, c/o Dip.
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Submitted (02-AUG-1993) Antonietta Palmisano, c/o Dip.
Submitted e Biologica, IABBAM CNR, Via Mezzocannone,16,
                                                                                                                Strongylocentrotus
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S.purpuratus DNA
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3 (bases 1 to 2347)
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                                                                                                                                                                                                                                                                                                                                                                                               585
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LGYTEAFKROTNSKKNMILGVGAYROTISGTGALRICASFLORFFKFSRDVFLPRP
TWGNNTFIFRDAGMQLOSYRYYDPKTCGFDETGALEDISKIPAGNYILLHACAHNPTG
TDRRREAMTVYKKNNLFAFFDMAYGGFASGDGNKDAWAVRHFIEQGINVCLCQSY
YAKNMGLYGERVGAFTVYCKDAEEAKRYESQLKILIRPWYSNPFINGARIASTILTSP
DLRKOWLHEVKGMADRIISMRTQLVSNLKKESSHNWQHIDQIGMFCYTGLKPEQVE
RLTKESTIYMTKOGRISVAGYVSGNVAYLAHAHHQVTK"

85 a 607 c 579 g 576 t
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/tissue_type="heart"
28. 87
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Napoli,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 2350)
Theze, N., Calzone, F.J., Thiebaud, P., Hill, R.L., Britten, R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Developmental appearance of factors that bind specifically to cis-regulatory sequences of a gene expressed in the sea urchin
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Echinodermata;
Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
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1274. .1282
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476. .500
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/dev_stage-"Embryo"
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1620. .1635
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1240. .1260
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1024. .1086
                                                                                                                                                                                                                                                                                     /bound_moiety="P8III"
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                                                                                                                                                                                                                                                                                                                                                /bound_moiety="P8I"
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456. .466
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427. .447
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Copenhagen K, Denmark
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Poulsen, P.
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X14233.1 GI:42720
pyrE gene; unidentified reading
Escherichia coli.
Escherichia coli
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Rndersen,J.T., Jensen,K.F. and Poulsen,P.
Role of transcription pausing in the control of the pyrE attenuator in Escherichia coli
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Ashida, M., Kawabata, T., Hirayasu, K. and Tsuchiya, M. Method for assaying activity of prophenoloxidase ac and application thereof
Patent: US 5585248-A 12 17-DEC-1996;
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132126
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A59593
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D25296
Rawasaki, T., Itoh, N. and Kawasaki, T. Rewasaki, T., Itoh, N. and Kawasaki, T. Gene organization and 5'-flanking region sequence of conglutinin: C-type mammalian lectin containing a collagen-like domain Biochem. Biophys. Res. Commun. 198 (2), 597-604 (1994)
                                                                   Submitted (18-NOV-1993) to the DDBJ/EMBL/GenBank databases. Nobuko Kawasaki, College of Medical Technology, Kyoto University: Kawaramachi 53, Shoyoin, Sakyo-ku, Kyoto, Kyoto 606-01, Japan (Tel:075-751-3934, Fax:075-751-3909)
                                                                                                                                                       Bos taurus mature liver nepatoryto pom.
Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae;
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                                                                                                                                                                                                                         conglutinin.
3 of 9
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/db_xref="taxon:32644"
32 c 29 g 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene, partial cds.
U65795
g1762792
                                                                                                                                                                                                                                                                                              Submitted (01-AUG-1996) Experimental Path., MN 55905, USA
                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 246)
Mathiesen, D. A and Persing, D. H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eubacteria; Spirochaetales; Spirochaetaceae; Borrelia.
1 (bases 1 to 246)
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           /Codon_start=2
/trans1_table=11
/product="outer surface protein A"
/product="outer surface protein A"
/protein_id="AAB39570.1"
/db_xref="pID:g1762793"
/db_xref="GI:1762793"
/db_xref="GI:1762793"
/trans1ation="IACKQNVSSLDEKNSVSVDLPGEMKVLVSKEKDKDGKYSLMATV
DNLELKGTSEKNNGSGVLEGVKADKSKVKLTVSEDLST"

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223. .>242
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                                                                                                                                                                                                                                  /organism="Borrelia burgdorferi"
/strain="AII"
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/dev_stage="mature"
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/db_xref="taxon:9913"
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|oin(D25294.1:571. .738,D25295.1:21.
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1 bp upstream of HindIII site.
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                                                                                                                                          Acrossochellus paradoxus.
Acrossochellus paradoxus
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Acrossochellus.

1 (bases 1 to 256)
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AJ011313
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Datta, U., Dutta, P. and Mandal, R.K
Cloning and characterization of a
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                                                                   Submitted (16-SEP-1998) Chiang T.Y., Department of Biology, Cheng-Kung University, Tainan, university Rd., TAIWAN 2, [bases 1 to 256]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Draft entry and printed copy of sequence R.K.Mandal, 02_JUN-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyprinus
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Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Cyprininae;
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M19418.1 GI:213062
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                                          Cloning HindIII satellite DNA of
                                                          Chiang, T.Y.
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Similarity 100.0%;
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Location/Qualifiers
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/db_xref="taxon:7962"
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Pred. No. 8.17e+03;
0; Mismatches (
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No. 8.17e+03;
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                                            Acrossocheilus paradoxus
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07-OCT-1997 (Rel. 52, Last updated, Version
Genomic RNA of hop stunt viroid type HSV-c.
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"METHOD FOR FRACTIONATING AND DETECTING HOP :
Patent number JP 1989040000-A/1, 10-FEB-1989
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Hop stunt viroid
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33 ttctcagaa 25
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Hop stunt viroid
JP 1989040000-A/1
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topology: Circular;
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05-AUG-1987 JP 1987194377
YOMO EISHIRO, SANO TERUO, KUDO HIROSHI, SUGIMOTO NOBUTAKA
C12Q1/70,C12N15/00,C12Q1/68,G01N33/50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-sense: No;
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L27299.1
                                                                                                                                           309 bp
Conepatus leuconotus
L27299
Mitochondrion Conepatus leuconotus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Carnivora; Fissipedia; Mustelidae; Conepatus
                                                                Conepatus leuconotus
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51 c
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/isolate="Wa23"
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/db_xref="taxon:12893"
64 A; 87 C; 81 G; 71 T; 0 o
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8.17e+03;
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8.17e+03;
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Racey,P.A. and Wayne,R.K.
DNA answers the call of pipistrelle bat s
Nature 387 (6629), 138-139 (1997)
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Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Mammalia; Eutheria; Chiroptera; Mic
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Dragoo, J.W., Bradley, R.D., Honey
Phylogenetic Relationships Among
                                                                                                                                                                                                                                                                                                                                                          Submitted (27-MAR-1997) Conservation G Zoology, Regents Park, London NW1 4RY,
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Barratt, E.M., Deavi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhinolophidae; Rhinolophus.
1 (bases 1 to 331)
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Similarity 100.0%;
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Location/Qualifiers
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/product="cytochrome b"
/product="cytochrome b"
/protein_id="AAC48750.1"
/db_xref="pid:g2253676"
/db_xref="G1:2253676"
/db_xref="G1:2253676"
/translation="ple:KIINDSFVDLPAPSSISSWWNFGSLLGICLAIOILTGLFLA
/translation="references"
/translation="ple:KIINDSFVDLPAPSSISSWWNFGSLLGICLAIOILTGLFLA
MHYTSDTATAFHSVTHICRDVNYGWVLRYLHANGASMFFICLFLHVGRGIYYGSYTFS
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Location/Qualifiers
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/db_xref="taxon:30543"
82 c 45 g
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                                                          No.
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                                                        DB 23; 1
8.17e+03;
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8.17e+03;
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Microchiroptera;
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U47049
g1199625
U47049.1 G
                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidea; Caprinae; Ovis.

1 (bases 1 to 374)

Hawken, R.J. and Maddox, J.F.
An ovine dinucleotide repeat polymorphism at the RJH1 locus Anim. Genet. 27 (3), 219-220 (1996)
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1 (bases 1 to 367)

Higgins,J.A., Radulovic,S., Schriefer,M.E. and Azad,A.F.
Rickettsia felis: a new species of pathogenic rickettsia isolated
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Direct Submission
                Hawken, R.J
                                                                                                                                                                                     sheep
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Similarity 100.0%;
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                           (bases 1 to 374)
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/transl_table=11
/product="citrate synthase"
/protein_id="AAB49576.1"
/db_xref="PID:g1015950"
/db_xref="GI:1015950"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"AHGGANEAVINMLKEIGSSENIPKFIAKVKDKNDPFRLMGFGHR
VYKNYDPRAAALKETCKAVLKELGQLENNPLLQIAIELEAIALKDEYFIERKLYPNVD
SHSGIIYKAMGIPSQMSTVL"
62 c 74 g 102 t
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<1. .>367
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/strain="JC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia akari strain-Kaplan.

Rickettsia akari
Eubacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.

1 (bases 1 to 383)

Higgins, J. A., Radulovic, S., Schriefer, M.E. and Azad, A.F.
Rickettsia felis: a new species of pathogenic rickettsia isoli
                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-DEC-1995) Abdu Azad, Microbiology and Immunology, University of Maryland at Baltimore, 655 W. Baltimore Street, Baltimore, MD 21201, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 383)
Azad, A., Higgins, J.A., Radulovic, S.
Direct Submission
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Rickettsia akari citrate
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J. Clin. Microbiol.
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/db_xref="taxon:9940"
/chromosome="9"
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                                                                                                                                                       /db_kref="g1:1145793"
/translation="wcgahgsaheavinmlkeigssenipkyiakakdksdpfrlmgf
/translation="wcgahgsaheavinmlkeigssenipkyiakakdksdpfrlmgf
ghrykknydprasulkeickevlkeigolennpllqiaieleaialkdeyfierklyp
nydfysgiiykamgipsqmftvlfa"
                                                                                                                                                                                                                                                                                                                            /organism="Rickettsia
/strain="Kaplan"
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53 c 67
                                                                                                                                                                                                                /product="citrate synthase"
/protein_id="AAB49577.1"
/db_xref="pID:g1145793"
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/transl_table=11
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d. No. 8.17e+03;
Mismatches 0;
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                                                                                          Length 383;
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Local Similarity 100.0%;
hes 9; Conservative
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X84524.1 GI:871645
X84524.1 GI:871645
16S ribosomal RNA; 16S rRNA gene.
unidentified bacterium.
unidentified bacterium
                                                                                                                                                                                                                                Bacteria; environmental samples.

1 (bases 1 to 396)

Bond, P.L., Hugenholtz, P., Keller, J. and Blackall, L.L.
Bacterial community structures of phosphate-removing and non-phosphate-removing activated sludges from sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-MAR-1997) A. Bhattacharya, Jawaharlal Nehru
University, School of Enviromental Sciences, New Delhi 110067,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIZ93401 385 bp
E.invadens rRNA gene
                                                                                                                                                                                                                                                                                                                                                                                               Unknown organism,
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Bhattacharya, A.
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1 (bases 1 to 385)
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Engineering, University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_
<1. .>3
               /organism="unidentified bacterium"
/db_xref="taxon:2338"
/clone_lib="mixed genomic 16S rDNA from activated sludge"
<1. >396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Trophozoite"
/cell_type="Trophozoite"
/clone_lib="ribosomal DNA"
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1. .385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="ribosomal RNA"
43 c 76 g 9
/gene="16S rRNA"
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/clone="INVD1"
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partial 16S rRNA gene
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                                                                                                                 Philip L. Bond, of Queensland, 1
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1. No. 8.17e+03;
Mismatches 0
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                                                                                                                 Department of Chemical Brisbane, Qld., 4072,
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Submitted (16-OCT-1996) Biology,
Submitted w 27599, USA
AF044660 402 bp DNA MAM 20-JAN-1
Rhinolophus hipposideros cytochrome b gene, mitochondrial
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Mansfleld,S.G., Cammer,S., Alexander,S.C., Muehleisen,D.P., Gray,R.S., Tropsha,A. and Bollenbacher,W.E. Molecular cloning and characterization of an invertebrate celretinoic acid binding protein retinoic acid binding protein proc. Natl. Acad. Sci. U.S.A. 95 (12), 6825-6830 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 399)
Mansfleld, S.G., Cammer, S., Alexander, S.,
Gray, R.S., Tropsha, A. and Bollenbacher, W.
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Manduca sexta cellular retinoic acid binding protein (mCRABP)
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/product="cellular retinoic acid binding protein"
/protein_1d="Aac24317.1"
/db_xref="ptD:g3115357"
/db_xref="GI:3115357"
/db_xref="GI:3115357"
/translation="MEFVGKKWISSENFDEFMKAIGVGLITRKAANAVTPTVELRQ
EGDGYNLVTSSTFKTTEMKFKPGEEFFDEERADGAKVKSVCTFEGNTLKQVQKAADGLE
VTYIREFGFEEMKAVWTAKDVTCTRVYKVQ"
102 c 121 g 72 t
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89 c 134
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/product="16S ribosomal
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33 ttctcagaa 25
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AF044660
g4159980
                               Submitted (23-NOV-1998) Microbiology, University Miguel Crta. valencia Km 87, Alicante, Alicante 03550, Spain Location/Qualifiers
                                                                                                                                           Appl. Env
99124582
                                                                                                                                                                                              Acinas, S.G., Anton, J. and Rodriguez-Valera, F. Diversity of free-living and attached bacteria in offshore western Mediterranean waters as depicted by analysis of genes encoding 16S
                                                                                                                                                                                                                                                                   uncultured gamma proteobacterium 400m-ATT-15.
uncultured gamma proteobacterium 400m-ATT-15
Bacteria; Proteobacteria; gamma subdivision;
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AF114520.1
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AF114520
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Universidad Complutense de Madrid, Facultad de Veterinaria, Ciudad
Universitaria s/n, Madrid 28040, Spain
Location/Qualifiers
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Bautista, J.M., Alvarez, Y. and Juste, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
2 /bases 1
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Chiroptera; Microchiroptera; Rhinolophidae; Rhinolophus
                                                                                     Acinas, S.G.
Direct Submission
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ILTGLFJAMHYTSDTDTAFFSVTHICRDVNYGWILRYLHANGASMFFICLFLHVGRGI
YYGSYTFSETWNIGIILLFAVMATAFWGYVLP"
126 c 57 g 107 t
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/protein_id="AAD05413.1"
/db_xref="PID:g4159981"
/db_xref="GI:4159981"
 /organism="uncultured gamma
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/transl_table=2
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proteobacterium 400m-ATT-15"
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AF063883
g3763468
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SHPMICB 470 bp DNA Ovis aries DNA microsatellite.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
Drosophilidae; Drosophila.
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Jordan, I.K. and McDonald, J.F.

Evolution of the copia retrotransposon
melanogaster species subgroup
Mol. Biol. Evol. (1998) In press
3 (bases 1 to 443)
                                                                                                                                                                                                                                                                                                                                                Submitted (08-MAY-1998) Genetics, Street, Athens, GA 30602, USA
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Jordan, I.K. and McDonald, J.F.
Inter-element selection in the
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                                                                                                                                                                                            /note="5' long terminal repeat LTR and region ULR"
21. .>443
/rpt_family="copia retrotransposon"
/rpt_type=dispersed
a 65 c 60 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /isolate="400m ATT"
/db_xref="taxon:86492"
/clone="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="uncultured attached marine bacterium recovered depth of 400m" ^{\circ}
                                                                                                                                                                                                                                                                            /organism="Drosophila
/db_xref="taxon:7243"
<1. .>443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="sequenced with reverse
/product="16S ribosomal RNA"
93 c 137 g 88 t
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                                                                                                                        Score 9; DB 22;
Pred. No. 8.17e+
0; Mismatches
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8.17e+03
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8.17e+03;
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long terminal
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1 (bases 1 to 470)

Hulme, D.J., Silk, J.P., Redwin, J. and Beh, K.J.

Ten polymorphic ovine microsatellites
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lymantria dispar
U04669
                                                                                                                                                            Submitted (21-DEC-1993) Robert F. Leclerc, University of Maryland, Center for Agricultural Biotechnology, Agriculture/Life Sciences Surge Bldg., College Park, MD 20742-3351, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 479)
Leclerc, R. F. and Regier, J. C.
Evolution of chorion gene families in lepidoptera: characterization
                                                                                                                                                                                                                                                                                                                                                                                                                              Lymantria dispar.
Lymantria dispar
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                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Lepidoptera; Noctuoidea;
                                                                                                                                                                                                                                                Leclerc, R.F
                                                                                                                                                                                                                                                                                                                                                                              Lymantriidae; Lymantria.
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                              cDNAs from the gypsy moth 1. Evol. 39 (3), 244-254 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Ovis aries"
/db_xref="taxon:9940"
complement(235. .258)
/note="PCR primer to amplify microsatellite; PCR primer binding site; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="PCR primer binding site; putative" 96 c 142 g 113 t 2 others
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/codon_start-1
                 /dev_stage="pupae"
<1. .420
                                                 /tissue_type="choriogenic follicles"
                                                                  /sex="female"
                                                                                                              /organism="Lymantria dispar"
/db_xref="taxon:13123"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /standard_name="reverse PCR primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="compound microsatellite; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .470
                                                                                clone_lib="choriogenic follicular cDNA"
                                                                                               clone-"Ld40"
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war clone Ld40
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d. No. 8.17e+03;
Mismatches 0;
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                                  496 k
Bovine cytochrome b
L22966 M63330
g387581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHKMCW8 491 bp DNA VRT Gallus domesticus DNA microsatellite marker MCW8 L40071
cytochrome
4 of 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 491)
Groenen, M.A.M., Crooijmans, R.P.M. and van der Poel, J.J.
Preliminary linkage map of the chicken (Gallus domesticus)
based on microsatellite markers: 77 new markers mapped
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA-microsatellite; polymorphic microsatellite.
Gallus gallus (clone: kl71) (tissue library: lambda ZAP) female adult blood DNA.
                           L22966.1
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Similarity 100.0%;
9; Conservative
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            GI:387581
ne b5; membr
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vasenvyegilaaagelpfvgtvgvegilptagagavyhscgdginamtsrdaafapr
fadavgiglgayglevpllnapalgyragwkgcgcgl"
479
                                                                                                                                                                                                                                                                            /rpt_family="CA-microsatellite"
419. .443
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="kl71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="chorion protein"
/protein_id="AAA67869.1"
/db_xref="PID:g454067"
/db_xref="GI:454067"
                                                                                                                                                                                                                                                                                                                               /tissue_type="blood"
/tissue_lib="lambda ZAP"
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132 c 129 g 14
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                                                                                                                                                                                                                                                                                                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
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Mismatches 0;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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hes 9; Conservative
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Heterodontus francisci tcr beta gene.
L47454
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Cristiano,R.J., Giordano,S.J. and Steggles,A.W.
The isolation and characterization of the bovine cytochrome b5
gene, and a transcribed pseudogene
Genomics 17 (2), 348-354 (1993)
                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L47454.1 GI:1032343
T cell receptor beta chain.
Heterodontus francisci (tissue library: lambda zap) adult spleen
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Bos taurus
 BS16SRMU
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Artiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                          Hawke, N.A., Rast, J.P. and Litman, G.W. Extensive Diversity of Transcribed TCR Primitive Vertebrate
                                                                                                                                                                                                                                                                                                                                                                                 Heterodontidae; Het
1 (bases 1 to 536)
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Chondrichthyes; Elasmobranchii; He
                                                                                                                                                                                                                                                                                                                                                                                                                                            Heterodontus francisci
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA to mRNA.
                                                                                                                                                                                     122
                                                                                                                                                                                                              /tissue_type="spleen"
/tissue_lib="lambda zap"
115. 536
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                                                                                                                                                                                                /partial
                                                                                                                                                                                                                                                     /organism="Heterodontus francisci"
/db_xref="taxon:7792"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="cytochrome
127 c 86 g
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/db_xref="taxon:9913"
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                                                                1 (bases 1 to 583) Caskey, C.T., Chamberlain, J.S., Gibbs, R.A., Rainer, J.E. and Nguyen, P.N.
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Tarvis,E.D., Cheng,S. and Rudner,R.

Genetic structure and DNA seguences at junctions involved in the rearrangements of Bacillus subtilis strains carrying the trpE26
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Bacillus subtilis
Bacteria; Firmicutes;
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X55333
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16S ribosomal RNA.
                                        Multiplex genomic DNA amplification for deletion detection Patent: EP 0364255-A2 12 18-APR-1990;
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/trans1_table=11
/protein_id="cah39032.1"
/db_xref="pID:9388215"
/db_xref="gI:388215"
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/organism="unknown"
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/translation="fryfrsfaiswidvelypfwansfkavsiisfsfsfngsilsep
ggllgkgiyqrlpdrnerigclspriff"
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                                    1 (bases 1 to 662)
Sager, R., Zou, Z., Lee, S.Whan and Tomasetto, C.Laure. Cancer diagnosis using nucleic acid hybridization Patent: US 5688641-A 16 18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l (bases 1 to 585)
COOPER, C.S. and Gusterson, B.A.
MATERIALS AND METHODS RELATING TO THE DIAGNOSIS
AND THERAPEUTIC TREATMENT OF SYNOVIAL SARCOMA
Patent: WO 9602641-A 5 01-FEB-1996;
                                                                                                             Unknown
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Other publication AU 2986595 960216.
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QYPNYPGGQGQYGGYRPTQPGPPPQPQRPYGYDQIMPKKPAEDENDSKGYSEASGP
QNDGKQLHPPGKANISEKIINKKSGFKRGKHAWTHRLRERKQLVIYEEISDPEEDDE"
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/db_xref="PID:e306311"
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conflict with the conceptual translation"
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T Biol. Chem. 263
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/db_xref="PID:d1039094"
/db_xref="PID:g4512599"
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join(AB023802.1:1. ...
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м86510.1
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SCHISTOSOMA mansoni glutathione peroxidase mRNA,
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Platyhelminthes;
Trematoda; Digenea; Strigeidida; Schistosomatoidea;
Schistosomatidae; Schistosoma.
MPB59; alpha antigen; antigen
            g1060915
D78142.1 GI:1060915
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/translation="MSSSHKSWNSIYEFTVKDINGVDVSLEKYRGHVCLIVNVACKCG
ATDKNYRQLOEMHTRLVSKGLRILAFFCNQFGGOEFWALAEIKKFVTEKYGVOFDMFS
KIKVNGSDADDLYKFLKSRQHGTLTNNIKWNFSKFLVDRQGQFVKRYSPTTAFYDIEG
                                                                                                                                                                                                                                                                                                                                                         DIMELLEKK"
                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_except=(pos:142...144,aa:Cys)
/product="glutathione peroxidase"
/protein_id="AAA29885.1"
/db_xref="PID:g160998"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Schistosoma
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1. No. 8.17e+03;
Mismatches 0
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antigen 85B, MPB59,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-OCT 1995) to the DDBJ/EMBL/GenBank databases. Naoya Ohara, Nagasaki University School of Dentistry, Oral Bacteriology; Sakamoto 1-7-1, Nagasaki, Nagasaki 852, Japan (E-mail:160202@cc. nagasaki-u.ac.jp, Tel:0958-49-7649, Fax:0958-49-7650)

2 (bases 492 to 738)
Matsuc,K., Yamaguchi,R., Yamazaki,A., Tasaka,H. and Yamada,T. Cloning and expression of the Mycobacterium bovis BCG gene for extracellular alpha antigen
J. Bacteriol. 170 (9), 3847-3854 (1988)
                 g915547
U32225.1
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Mycobacterium bovis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                         TAU32225 768 bp DNA INV 01-AUG-1995
Theileria annulata cytochrome oxidase polypeptide III (coxIII) gene, mitochondrial gene encoding mitochondrial protein, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Characterization of the transcriptional initiation regions of for the major secreted protein antigens 85C and MPB51 of Mycobacterium bovis BCG microb. Pathog. 23 (5), 303-310 (1997)
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/transl_table=11
/product="alpha antigen, a
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509. .514
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237 c 226 g 135 t
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strain="BCG Tokyo"
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83. .>738
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1 (bases 1 to 789)
1 (bases 1 to 789)
1 Beyer, J.C., Stich, R. W., Hoover, D.S., Brown, W.C. and Cheevers, W.P. Cloning and expression of caprine interferon-gamma Gene 210 (1), 103-108 (1998)
98192545
                                                                                                                                                                                                                                            goat.
2 (bases 1 to 789)
Beyer, J.C. and Cheevers, W.P.
Direct Submission
Submitted (17-AUG-1995) Joseph C. Beyer, Veterinary Microbiology
and Pathology, Washington State University, Bustad Hall, Pullman
                                                                                                                                                                                                                                                                                                                    Capra hircus
U34232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 768)
Lawson,D. and Hall,R.
Synonymous codon usage
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Eukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa;
Piroplasmida; Theileriidae; Theileria.
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2 (bases 1 to 768)
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/product="cytochrome oxidase polypeptide III"
/protein_id="AaA73631.1"
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FSTFINGFFHFRLSNPVMIIEVNLEAFIQISDVLNAGSILISLILQRIEERGYFEVDY
RUBRLILIGFTFLSFOGDEYSLVKSYINNHWYTLYFNVLTGLHSLHYVVGGIFALMQA
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1 84 c 116 g 302 t
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/EC_number="1.9.3.1"
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/mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Hissar"
/db_xref="taxon:5874"
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8.17e+03;
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Jarvis, E.D., Cheng, S. and Rudner, R.
Genetlc structure and DNA sequences at junctions involved in the
rearrangements of Bacillus subtilis strains carrying the trpE26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16S ribosomal RNA.
Bacillus subtilis.
Bacillus subtilis
Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
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/trans1_table=11
/protein_id="CAA39031.1"
/db_xref="PID:9388214"
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                                                       /note="P2 580. .585
                                                                                                                                                              460.
                                                                                        /note="P1 promoter" 557. .562
                                                                                                                                                                           /db_xref="SWISS-PROT:004385"
/taanslation="Affeanofidaynavvhalhhlarievidrgfhpettvwsovrq
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MEPOVYKLYSELIESHESLEKRIELILFLANDFLIHSKAEIGSAHLFEVWKEKOJWQFG
ELLQHHDLKHFTQDLGVMLDYLTEKGLINVCQIETKGQAVYHRGYSFKKGVDSDS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="interferon-gamma"
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/db_xref="GI:1730274"
                     /note="P2 promoter"
767. .>808
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bacillus subtilis"
/strain="168-type"
/db_xref="taxon:1423"
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   /note="rrnD ribosomal operon"
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Matches 9; Conservative
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AJ223315.1 GI:2879887
allergen; rAsp f 7.
allergen; rAsp f 7.
Aspergillus fumigatus.
Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota; Euascomycetes; Plectomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 855)
Oligonucleotide.
A25392
g833582
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AJ223315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-FEB-1998) Hemmann S., Molecular Allergology, Swiss Institute of Allergy and Asthma Research (SIAF), Obere Strasse 22. CH-7270 Dayos, SWITZERLAND
                                           A25392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant Aspergillus fumigatus allergens: from the sequences to clinical applications Int. Arch. Allergy Immunol. 115 (2), 99-114 (1998)
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                           /codon_start=1
/codon_start=1
/product="rAsp f 7"
/protein_id="CAB11255.1"
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/db_xref="GISB879888"
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162 c 1
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/strain-"ATCC 42202"
/db_xref-"taxon:5085"
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J. Biol. Chem. 263, 11126-11129 (1988)
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1 (bases 1 to 900)

2heng,D.B., Lim,H.M., Pene,J.J. and White,H.B.III.

Chicken riboflavin-binding protein: cDNA sequence and homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus
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Chicken (White leghorn, adult female)
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                                                                                                                                                                                                                                                                                                                     /organism="Gallus gallus"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                       /note="riboflavin-binding protein signal peptide"
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zessccyanfteolafspiikvsnsymnrcgolskscebfikkiecfyrcsphaarmi
DPRYTAA1OSVPLCOSfcDDWYEACKODSICAHMILTDWERDESGENHCKSKCVPYSE
WYANGTDMCQSMWGESFKVSESSCLCLOMNKKDMVAIKHLLSESSEESSSMSSSEEHA
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    206 c 228 g 220 t
                                                                                /note="riboflavin-binding protein"
196 c 231 g 205 t
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Tetrahymena pyriformis
Tetrahymena pyriformis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 933)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding low-M(T) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena thermophila and amicronucleated Tetrahymena pyriformis Gene 144 (1), 123-125 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (27-0CT-1993) to the DDBJ/EMBL/GenBank databases.
Submitted (26-0CT-1993) to the DDBJ/EMBL/GenBank databases.
Koh-ichi Nagata, Gifu University School of Medicine, Department of Biochemistry; 40 Tsukasamachi, Gifu, Gifu 500, Japan (Tel:0582-65-1241(ex.2230), Fax:0582-65-9002)
2 (bases 1 to 933)
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Tetrahymena pyriformis (strain:W) cDNA to mRNA, clone_lib:lambda
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Tetrahymena pyriformis
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220 c
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/translation="MVDNKQDVAEFKLVLVGDGGVGKTTFVTRHQTGEFEKRYIATQ
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PFLWILRKLTGDPNLNLVEGIALAPVDIHMTEDQIKQLQMEHDEAMNLAQQGQLPDEE
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                                                                                                                                                                                                                                                                                                                                     /product="Ran/TC4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:5908"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Tetrahymena
/strain="W"
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/transl_table=6
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                                                     Providencia stuartii plasmid VR-1 beta-lactamase TEM-60) gene, complete cds.
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3 of 9
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Providencia stuartii
Providencia stuartii
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                                  AF047171.1
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Gene 193 (2), 219-227 (1997)
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/gene="GC-E"
/number=7
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/tissue_type="retina"
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/number=7
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/strain="Holstein dairy cow"
/db_xref="taxon:9913"
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Matches 9; Conservative
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Perilli,M., Felici,A., Franceschini,N., De Santis,A., Pagani,L.,
Luzzaro,F., Oratore,A., Rossolini,G.M., Knox,J.R. and Amicosante,G.
Characterization of a new TEM-derived beta-lactamase produced in a
Serratia marcescens strain
Antimicrob. Agents Chemother. 41 (11), 2374-2387
Direct Submission
Submitted (12-APR-1996) M. Perilli, Dipartimento di Scienze
Technologie Biomediche e Biometria, Universita dell'Aquila,
                                                                                                                                                                                                                                                                                                                              Serratia marcescens
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                        x97254.1 GI:2648042
beta-lactamase.
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                                                                              Perilli, M.
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227 c
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ISLDNGGKIILESFREELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHYTRL
DSWEPELNEAIPNDERDTTMPAAMRTTLRKLLTGELLTLASRQQLIDMMEADKVAGPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="beta-lactam hydrolase;
spectrum beta lactamase (ESBL)
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Submitted (24-OCT-1997) Laboratoire de Biologie Cellulaire,
Universite Paris Sud, Bat. 444, Orsay 91405, France
Location/Qualifiers
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                                                                                                                         /gene="HSP70"
/product="heat shock protein 70"
<1. .>1047
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/gene="HSP70"
/codon_start=1
/transl_table=10
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                                                                                                 /gene="HSP70"
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/db_xref="taxon:5940"
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Boyd, E.F. and Hartl, D.L.
Boyd, E.F. and Hartl, D.L.
Boyd, E.F. and Hartl, D.L.
Boversifying selection governs sequence polymorphism in the major adhesin proteins FimA, PapA, and SfaA in Escherichia coli
J. Mol. Evol. (1999) In press
2 (bases 1 to 1050)
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Escherichia coli strain ECOR 52 major pilin protein precursor
(papA) and PapH (papH) genes, partial cds.
AF051814
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SPEEISAMILVKMKQIAENYLGOEVKNAVITVPAYFNDAQRAATKDAGIISGLNVLRI
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                                                                                                                                                                                                     /translation="PMAVVSFGVNAAPTIPQGQGKVTFNGTVVDAPCSISQKSADQSI
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                                                                                                                                                                                  GAFSAVANFNLTYO"
                                                                                                                                                                                                                                                                                  /product="major pilin protein
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/db_xref="PID:g4106022"
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/protein_id="AAC33417.1"
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Pred. No. 8.17e+03;
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498 TTCTCAGAA 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arlet,G., Goussard,S., Courvalin,P. and Philippon,A. Sequence of the genes for TEM-20, TEM-21, TEM-22 and extended-spectrum beta-lactamases
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-lactamase class A. Klebsiella pneumoniae. Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPY17583 1071 bp DNA BCT Klebsiella pneumoniae blaTEM-22 gene, partial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-JUN-1998) G.J. Arlet, Hopital Saint-Louis Microbiologie, 1 Avenue Claude Vellefaux, 75475 Paris Cedex 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                   similarity 100.0%;
9; Conservative
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a 203 c 286 g 307 t
                                                                                                                              LRSALPAGWFIADKSGGSERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
EIGASLIKHW"
1 234 c 263 g 281 t
                                                                                                                                                                                 /product-"beta-lactamase class A".
/protein_id-"CAA76795.1"
/protein_id-"CAA76795.1"
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IELDLNSGKILESFRPEERFPMMSTEKVLLGGAVLSRVDAGOEQLGRRIHYSQNDLVK
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DRWEPELNBAIPNDERDTTMBAAMATTIKKLLTGELLTLASRQQLIDWMBADKVAGPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Klebsiella
/strain="SLK52"
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                                                                                                                                                                                                                                                                                                                                                                                               /gene="blaTEM-22"
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                                   e 9; DB 17; Leg
. No. 8.17e+03;
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. No. 8.17e+03;
Mismatches 0;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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I31987
                                                                    g1822778
I31987.1
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2 (bases 1 to 1079)
Johnsen, L.B., Poulsen, K., Kilian, M. and Petersen,
Jurification and cloning of a streptokinase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (15-DEC-1998) Johnsen L.B., Molecular and biology, University of Aarhus, Gustav Wieds vej 10C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus uberis. Streptococcus uberis
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AJ131631.1 GI:4033580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="steptokinase"
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/db_xref="gl:4033581"
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IVDFAPDAQLLTRDRRTLFANRWFEESVSLEDTIQEXLLKGHVILKRKVEEPITHPTE
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JANIEYKVQFATKGGERHPLPITWOYGEKHIGEKLTSDEFRKIAEEKLIGSYDDYMID
JANIEYKVQFATKGGERHPLPITWOYGEKHIGEKLTSDEFRKIAEEKLIGSYDDYMID
JANIEYKVQFATKGGERHPLPITWOYGEKHIGEKLTSDEFRKIAEEKLIGSYDDYMID
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JANIEYKVQFATKGGERHPLPITWOYGEKHIGEKLTSDEFRKIAEEKLIGSYDDYFEK
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173 c 174 g 348
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256. .1038
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/isolate="9756-296-LF"
/db_xref="taxon:1349"
181. .255
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181. .]
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                                                                     GI:1822778
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/transl_table=11
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Pred. No. 8.17e+03;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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E08994;
E08994.1
E08994.1
    TAKARA
OS NO
OC Ar
PN JP
PD 04
PF 16
PR 20
PI OK
                                                                                                                                                                                                                                                                                                         07-OCT-1997 (Rel. 52, Created)
07-OCT-1997 (Rel. 52, Last updated, Version 1)
DNA encoding an immunogenic peptide derived from human influenza virus haemaglutinin that doesn't have globular region.
JP 199508999-A/4.
unidentified
unclassified.
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                                                                                                                                                                                       Okuno Y., Isekawa Y., Sasao F., Ueda S.;
"IMMUNOGENIC ARTIFICIAL POLYPEPTIDE";
Patent number JP 1995089992-A/4, 04-APR-1995.
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Artificial sequences.
JP 1995089992-A/4
04-APR-1995
16-MAR-1994 JP 1994070194
20-APR-1993 JP 93P 115216
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  OKUNO YOSHINOBU, ISEKAWA YUJI,
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Richards,S., Kaplan,J. and Moscicki.
Prolactin as a vaccine adjuvant
Patent: US 5585099-A 2 17-DEC-1996;
Location/Qualifiers
                                                                                                                                                                   SHUZO CO LTD.
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Lesslauer, W., Lotscher, H. and Stuber, D.
TNF-muteins
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Location/Qualifiers
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(C12P21/02,
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Venkateswarlu,K. and Cullen,P.J.
                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-FEB-1999) Venkateswarlu K., University of Bristol, School of Medical BS8 1TD, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ236896.1 GRP1 protein
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                                                                                                                                                                                                                                                                                                               Unpublished
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/product="GRP1 protein"
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/protein_id="CAB38534.1"
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/db_xref="piD:9481795"
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/db_xref="GI:4481795"
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PFALETLDRFTKEHKLHDVPIVPALROYLFSTRPPGESQKINNILEKGAEVYANQNS
YGNADQAHTVAYSCIMVNTLLHNPNVKDKPSLEKYIEMNEQLLEKGAITIEQLTEVYE
SYSTTOFKIPDEVSTSGKGTVNDILLHAEREGWLFKQSSNPLFSGALSWKKRWFVLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:32644"; 374 A; 216 C; 258 G;
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                                                                                                                                                                     /function="GTP-exchange factors"
                                                                                                                                                                                                                                                        /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
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                                                                                                                                           'codon_start=]
                                                                                                                                                          'note="general receptor
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                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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g2995746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cracraft, J., Feinstein, J., Vaughn, J. and Helm-Bychowski, K. Sorting out tigers (Panthera tigris): mitochondrial sequen nuclear inserts, systematics, and conservation genetics Anim. Conserv. 1, 63-74 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion Panthera tigris
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Carnivora; Fissipedia; Felidae; Panthera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-MAR-1998) Ornithology, History, 79th at Central Park West, 1
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SSPAG201 1204 bp DNA MAM Sus scrofa pregnancy-associated glycoprotein
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                                                                                                                                                                                                                           /product "cytochrome b"
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rehpytytikdiiglivlititlivlfyfpalliopdnyipanpinnpehikpewyfif
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/transl_table=2
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/mitochondrion
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/isolate="S3"
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(pPAG2) gene, pro
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NY 10024, USA
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U39198
g1223870
U39198.1
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Submitted (23-OCT-1995) Bozena Szafranska, Animal Sciences,
University of Missouri-Columbia, 158 ASRC, Columbia, MO 65211,
Szafranska B. Biol.Reprod 53, 21-28, 1995.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            PROTECTIVE PEPTIDE ANTIGEN
Patent: WO 8402922-A 7 02-AUG-1984;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthetic construct artificial sequence.
1 (bases 1 to 1212)
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A04190.1 GI:344796
fusion protein.
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Artificial sequence for galactosidase fusion
P.knowlesi CS protein immunogenic region.
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Szafranska,B., Xie,S., Miura,R. and Roberts,R.M.
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Sus scrofa
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/note="5', flanking region o
/db_xref="taxon:9823"
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a 309 c 252 g 318 t
                                                                                       /db_xref="GI:344797"
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DRWEPELNEAIPNDERDTTMPAGGGGGGGDGANAGQPQAQGDGANAGQPQAQGDGAN
AGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGQPQAQGDGANAGPPPPPPAAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGF
LLRSALPAGWETIADKSGAGERGSRGIIAALGPDGKPSRIVYIYTTGSQATMDERNRQI
AEIGASLIKHW"
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/transi_table=11
/product="galactosidase fusion protein"
/protein_id="cAA00346.1"
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Local Similarity 100.0%;
hes 9; Conservative
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U59717
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Direct Submission
Submitted (03-JUN-1996) Faculte de Medecine, Unite des Rickettsies,
Submitted (03-JUN-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP J0054, 27, bd Jean Moulin, 13385 Marseille Cedex 5, France
Location/Qualifiers
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U59717.1
                 Trypanosoma cruzi.
Trypanosoma cruzi
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AJ006226
                                                   antioxidant; mpx gene;
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Rickettsia akari
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                        ÃJ006226.1 GI:3393045
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Raoult, D., Rydkina, E., Roux, V., Eremeeva, M. and Balayeva, N.
Phylogenetic Analysis of the genus Rickettsia by Citrate Synthase
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IRMIAKIPTIAAMSYKYSIGQPFYYDNSLDFTENFLHMMFATPCTK/KNNPIIKNAL
IRMIAKIPTIAAMSYKYSIGQPFYYDNSLDFTENFLHMMFATPCTK/KNNPIIKNAL
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IGSSENIPKYIAKAKDKSDPFRLMGFGHRVYKNYDPRASVLKETCKEVLKELGQLENN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="MK(Kaplan)"
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carbamate kinase; carbamoyl-phosphate synthetase;
Pyrococcus furiosus.
Pyrococcus furiosus
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Direct Submission
Submitted (05-DEC-1996) V. Durbecq, Laboratoire de Microbiologie
ULB and Institut de recherches du CERIA, 1 Av. Emile Gryson, 1070
                                                                                                     Durbecq,V., Legrain,C., Roovers,M., Pierard,A. and Glansdorff,N. The carbamate kinase-like carbamoyl phosphate synthetase of the hyperthermophilic archaeon Pyrococcus furiosus, a missing link in the evolution of carbamoyl phosphate biosynthesis proc. Natl. Acad. Sci. U.S.A. 94 (24), 12803-12808 (1997)
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                                                   Durbecq, V
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furiosus cpkA gene
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385. .91
/gene="mpx"
/product="peroxiredoxin"
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/protein_id="CAA06923.1"
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274 . . 384
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HIV binding; MHC class II molecule binding;
glycoprotein; transmembrane protein
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Revised by author 04-SEP-97
On Sep 9, 1997 this sequence version replaced gi:1743371.
                                                                                                          Milde,K.F., Conner,G.E., Mintz,D.H. and Alejandro,R Primary structure of the canine CD4 antigen Biochim. Biophys. Acta 1172 (3), 315-318 (1993)
                                                                                                                                                                                                        Direct Submission Submitted (05-OCT-1992) K.F.
                                                                                                                                                                                                                                                                                                       Canis familiaris
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Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                           Diabetes Research Institute
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KVLAALRFIEWGERAIIAHLEKAVEALEGKTGTQVLP*
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KRGMEKKVVTIIITQTIVDKNDPAFQNPTKPVGPFYDEETAKRLAREKGWIVKEDSGRG
WRRVVPSPDPKGHVEAETIKKLVERGYIVIASGGGGVPYILEDGEIKGVEAVIDKDLA
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/strain="Beagle"
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                                                                Location/Qualifiers
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strain-"DSM 3638"
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Dierkes, B., Kriegesmann, B., Baumgartner, B.G. and Brenig, B.
Partial genomic structure of the bovine PIT1 gene and
characterization of a Hinfi transition polymorphism in exon
Anim. Genet. 29 (5), 405 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus PIT-1 gene,
                                                                     The pituitary-specific transcription factor GHF-1 homeobox-containing protein Cell 55 (3), 505-518 (1988)
                                                                                                                                                                Goettingen, FRG
3 (bases 1 to 1301)
                                                                                                                                                                                                    Submitted (22-DEC-1997) B. Kriegesmann, Institute of Veterinary Medicine, Molecular Biology, Groner Landstrasse 2, 37073
                                                                                                                                                                                                                                           Kriegesmann, B.
Direct Submission
Moody, D.E., Pomp, D. and Barendse, W.
                                                                                                                                              Bodner,M., Castrillo,J.L., Theill,L.E., Deerinck,T., Ellisman,M.
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovinae;
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/note="transmembrane domain"
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599. .898
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LNLKEQAAKVSKQQKLVWVVDPEGGTWQCLLSDKDKVLLASSLNVSSPVVIKSWPKFL
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                                                                                                                                                                                                                                                                                                                                                                                 208 TTCTGAGAA 216
                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                            B. Eaurus mRNA for conglutinin.
X71774
                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. 1 (bases 1 to 1305)
Lu, J., Laursen, S.B., Thiel, S., Jensenius, J.C. and Reid, K.B.
The cDNA cloning of conglutinin and identification of liver as a primary site of synthesis of conglutinin in members of the Bovidae Blochem. J. 292 (Pt 1), 157-162 (1993)
Reid,K.B.M.
Direct Submission
Submitted (23-JUL-1993) K.B.M. Reid, MRC Immunochemistry Unit,
                                                                                                                                                                                                 Bos taurus.
                                                                                                                                                                                                                 conglutinin.
                                                                                                                                                                                                                               g395267
X71774.1 GI:395267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anim. Genet. 26 (1), 45-47 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                               h 100.0%;
Similarity 100.0%;
9; Conservative
                                               (bases 1 to 1305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /citation=[3]
/replace="a"
1282..1301
/gene="PIT-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"growth hormone factor
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/db_xref="pin:e13766421"
/db_xref="gi.3766421"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(<1. .52,1092. .>1301)
/gene="PIT-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
/db_xref="taxon:9913"
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/note="allele
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EELNLEKEVVRVWFCNRRQREKRVKTSLNQSLFTISKEHLECR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )oin(<1. .52,1092. .>1301)
/gene="PIT-1"
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| 1993 | gene="PIT-1"
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Pred. No. 8.17e+03;
0; Mismatches 0
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109391
9587921
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Dryja, T. P., Friend, S. and Yandell, D.W.
DIAGNOSIS OF RETINOBLASTOMA
Patent: WO 8906703-A 24 27-JUL-1989;
                                                      A.velutinum
277768
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gene.
                          g1769911
z77768.1 GI:1769911
                                                                                                                                                                                                                                                                                                                                                                                               Unknown
           petD gene;
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NALKQRYTILDGHLRRFQNAFSQYKKAVLFPDGGAVGEKIFKTAGAVKSYSDAVQLCR
EAKGQLASPRSGAENAVTQMVRAQCEKNAYLSHNDISTEGRFTYPTGEILVYSNWADG
EPNNSDEGQPENCVEIFPDGKWNDVPCSKQLLVICEF*
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/translation="MLLPLT-VELTLTOPWRSLGAEMTTFSQKILANACTLVMCSPLE
SGLFGHDGQDGAECHKEEKSDDGSFGFAGRAGREGWVGFIGPKGDNGYVGEFGFRGDT
GPRGPPGMPGPAGREGPSGKQGSMGPPGTPGPKGETGPKGGVGAPGIQGFPGPSGLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="conglutinin"
340 c 405 g
                                                                                                                                                                                                                                                                /organism="unknown"
192 c 219 g
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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db_xref="taxon:9913"
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             ribosomal protein 11; RNA polymerase;
                                                                  1346 bp
chloroplast
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Pred. No. 8.17e+03;
0; Mismatches 0
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Pred. No. 8.17e+03;
0; Mismatches 0
                                                                    rpoA gene
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          rpoA gene; rps11
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Chloroplast Australopyrum velutinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukhryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Australopyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-JUL-1996) G. Petersen, Botanical Institute, Botanical Laboratory, Gothersgade 140, Dk-1123 Copenhagen K, DENMARK
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Petersen,G. and Seberg,O.
Phylogenetic analysis of the Triticeae (Poaceae) based on
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                                                                                                                                                                             472
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/db_xref="PID:e256589"
/db_xref="PID:97169914"
/db_xref="FID:91769914"
/db_xref="SPTREMBL:P39992"
/translation="KSLTIGLE"
a 220 c 248 g 404 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="alpha subunit c
/protein_id="CAB01381.1"
/db_xref="PID:e256852"
/db_xref="PID:91769912"
/db_xref="PID:1769912"
                                                                                                                                                                                                                                                                                                                                                                      /gene="petD"
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                                                                                                                                                                                                                                                                                                                                                       complement(1320. .>1346)
                                                                                                                                                                                                                                                                                                                                 /gene="petD"
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)6. .1115
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/db_xref="PID:g1769913"
/db_xref="GI:1769913"
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/product="ribosomal protein 11"
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'dev_stage="adult"
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/isolate="H6724"
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Pred. No. 8.17e+03;
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                g156239
M205011 GI:156239
CeRep3 repeat; repeat region.
C.elegans DNA, clone CeRep3.2.
   Caenorhabditis elegans
                                                                                                           C.elegans CeRep3 repe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manduca sexta
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hastings,R.A., Dawson,S.P., Billett,M.A. and Mayer,R.J. The regulatory ATPases S10b is not only present in the 26S proteasome but also in a smaller 220 kDa complex and as free molecules in the intersegmental muscles of the tobacco horn moth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JAN-1998) Hastings R.A., School of Biomedical Sciences, University of Nottingham, Medical School, Queen's Centre, Nortingham, Norts, NG7 2UH, UK
2 (bases 1 to 1346)
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/translation="MPAGPSAVDTPREKAFQDYRKKLMEHKEVESRLKAMRDQLKDLT/translation="MPAGPSAVDTPREKAFQDYRKKLMEHKEVGGRQLDKINKLKGG
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TRVALDMTTLTIMRHLPREVDPLYYNMSHEDPGDYTYAAIGGLQEQIQDREVIELPL
LNPELFYRVGITPPKGCLLYGPPGTGKTLLARAVASQLDANFLKVVSSAIVDKYIGES
ARLIREMFNYARDHQPGIIFMDEIDAIGGRREFEGTSANEIQRTLMEHLNQMDGFDS
ARLIREMFNYARDHQPGIIFMDEIDAIGGRREFEGTSATLEILKIHAAFIAKHGEMD
LGQVKIIMATNRPDTLDPALLRGGRLDKKIEIPLPNEQARLEILKIHAAFIAKHGEMD
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/db_xref="taxon:7130"
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88174732
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Bird.L.E. and Wigley,D.B.
Direct Submission
Submitted (11-NO-1998) Sir William Dunn
University of Oxford, South Parks Road, O
Location/Qualifiers
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Felsenstein,K.M. and Emmons,S.W.
Felsenstein, E.M. and Emmons, S.W.
Nematode repetitive DNA with ARS as
Saccharomyces cerevisiae
Saccharomyces cerevisiae
Mol. Cell. Biol. 8, 875-883 (1988)
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Secernentea; Rhabditia; Rhabditida; Rhabditina;
Rhabditidae; Caenorhabditis.
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The Bacillus stearothermophilus replicative helicase: cloning,
overexpression and activity
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Bacillus stearothermophilus
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/db_xref="gI:4416322"
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249 c 281 g 333 t
              FALNIAQNVATKTNENVAIFSLEMSAQQLVMRMLCAEGNINAQNLRTGKLTPEDWGKL
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RQQEVSEISRSLKALARELEVPVIALSQLSRSYEQRQDKRPMMSDIRESGSIEQDADI
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                                                                  /translation="MSELFSERIPPOSIEAEOAVLGAVFLDPAALVPASEILIPEDFY
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NIKDILVQTYDNIEMLHNRDGEITGIPTGFTELDRMTSGFQRSDLIIVAARPSVGKTA
VAFLYRDDYYNKDSENKNI I E I I I AKQRNGPVGTVQLAF I KEYNKFVNLERRFDEAQ I
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/note="5'- 3'
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/strain="NCA1503"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-JUN-1994) William M. Gelbart, Cellular and
Developmental Biology, Harvard University, Biological Laboratories,
16 Divinity Avenue, Cambridge, MA 02138, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caencrhabditis elegans
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetic characterization and cloning of mothers against dpp, a gene required for decapentaplegic function in Drosophila melanogaster Genetics 139 (3), 1347-1358 (1995)
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/LENLEEPALRCQGQQKTECVTIPRSLDGRLQISHRKALPHVIYCRYEWPDLQSHHELK
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IFDMEIFRQLLEDCSRRGEDASFDLQKMTFIRMSFYKGWGAEYQRQDVTSTPCWIEIH
LHAPLAWLDRVLSTMGPTPRPISSIS"

382 t
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45. .1301
                                                                                                                                                                                                                                                                  /note="similar to Drosophila melanogaster MAD polypeptide,
GenBank Accession Number U10328"
                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="mixed stage cDNA library (Barstead Waterston, 1989)"
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/db_xref="PID:g551487"
/db_xref="GI:551487"
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/db_xref="taxon:6239"
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Prince, V.E., Joly, L., Ekker, M. and Ho, R.K.
Zebratish hox genes: genomic organization and modified colinear expression patterns in the trunk
Homo sapiens
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/db_xref="GI:2661827"
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TPSPFPAQTEQCPAVQISGSRTCGQQQNTKTQNGIPTKQPAVVYPMKKVHVTTVNPD
YTGPPEKRSRTAYTRQQVLELEKEFHFNRYLTBRRRIESAHTLSLSERQIKIWFQNRR
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/db_xref="taxon:7955"
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                                                                                                                             Submitted (03-MAY-1995) Oxelman B., Department of Systematic Botany, Carl Skottsbergs Gata 22, S-413 19, Gothenburg, SWEDD 3 (bases 1 to 1429)
Oxelman, B. and Liden, M. Generic boundaries in the tribe Sileneae (Caryophyllaceae) as inferred by nuclear rDNA sequences
Taxon 44, 525-542 (1995)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Caryophyllidae; Caryophyllales; Caryophyllaceae; Agrostemma.
1 (bases 1 to 142)
Oxelman B. and Liden,M.
Generic bundaries in the tribe Sileneae (Caryophyllaceae) as
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X86895.1 GI:798816
28S ribosomal RNA; 5.8S ribosomal RNA; internal transcribed spacer
1; internal transcribed spacer 2; ITS1; ITS2.
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x86895
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CAEEARKKINSWYKTOTKGKIPMILPEGSYDGDTMYLVNAVYERGKWKTPEEKKLNS
LYPFRVNSAORTPVOMYLREKUNIGYIEDLFAAOILELPYAGDVSMFLLHDEIADVS
TGLELLESEITYDKLNKWTSKOKMAEDEVEVYIPOFKLEEHYELRSILRSMGMEDAFN
KGRANFSGMSERNDLFLSEYFHQAMVDVNEEGTEAAAGTGGVMTGRTGHGGPQFVADH
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/organism="Agrostemma githago"
/note="species author is L."
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/codon_start=1
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Submitted (28-APR-1994) to the DDBJ/EMBL/GenBank databases. Tateo Itoh, Osaka University, Faculty of Science, Department of Biology;
1-1 Machikaneyama-cho, Toyonaka, Osaka 560, Japan
[E-mail:c62528a@center.osaka-u.ac.jp, Tel:06-850-5432(ex.4307),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECOCOLEZIC 1457 bp I
Escherichia coli plasmid
encoding Rep protein.
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2 (bases 1 to 1457)
Hiraga,S., Sugiyama,T. and Itoh,T.
Comparative analysis of the replicon regions
ColE2-related plasmids
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/product="Rep protein"
/protein_id="BAR06296.1"
/db_xref="PID:01006800"
/db_xref="PID:9809455"
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                                                                                     /translation="msaalqyfeenlphrpyhtddlafglriggkgrallaryiqonq phaqfwlyfyddregaaidwsdrnaparnityknpunghahllaryidelaayi kalkiaavtapdasy kalkyaaversiceklcadvusglickpfhlewlywewreeaytldeladyidls asarrsidkhygmgrnchlfemtrwayrairgfhoympapsowldavigrvemynaslpy plsppecraigksiaxythrnptpetpaqyvadthtpetqakrgrkggiakgeaydbk rfmalcmlengysgkaiaamlevstrtirnwksgk"
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382. .615
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/db_xref="taxon:39848"
/tissue_type="fresh leaf"
                                                                                                                                                                                                                                                                                                                                              /organism="Escherichia coli"
/plasmid="Plasmid ColE2imm-K317"
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Enterobacter intermedius.
Enterobacter intermedius
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Osborn, A.M., Pickup, R.W. and Saunders, J.R.
Plasmid replicons, from lakewater sediments, homologous to the pGSH500 beta replicon are members of a larger group of classA theta replicons widely distributed in bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (31-JUL-1998) Osborn Division of Microbiology, GBF, D-38124, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osborn, A.M., da Silva-Tatley, F.M., Steyn, L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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/db_xref="PID:e1363554"
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/db_xref="GI:4127798"
                                                                                                                     /gene-"tapA"
421. .498
                                                                                                                                                    /function="antisense control" complement(317. .403)
/gene="coph"
421. .498
                                                                                                                                                                                                                        complement(317. .>403)
                                                                                                                                                                                                                                  /translation="NPMTASEKQLAAVARKRITHKEVKVFIRNPLKDRMIALCDQEGI
TQAQFIEKLIERELSEQGLLK"
                                                                                                                                                                                                                                                                                                                                                                         'gene="copB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Enterobacter intermedius"
/plasmid="pLV1402"
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l. .1477
                                                                  'codon_start=1
'transl_table=11
                                                                                                          'gene="tapA"
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1 (bases 1 to 1482)

Goss,N.H. and Richardson,M.A.

Variants of PAI-2

Location/Qualifiers

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                                                                                                                                        complete sequence. AF114501
                                                                                                                                                                       AF114501 1489 bp DNA BCT 12-MAR-1999 Uncultured gamma proteobacterium SUR-ATT-18 16S ribosomal RNA gene.
              Bacteria; Proteobacteria; gamma subdivision; environmental samples.

1 (bases 1 to 1489)
                                                 uncultured gamma proteobacterium SUR-ATT-18 uncultured gamma proteobacterium SUR-ATT-18
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Acinas, S.G., Anton, J. and Rodriguez-Valera, F
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
307 c 320 g
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/protein_id="CAA08930.1"
/db_xref="PID:e1363555"
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Matches 9; Conservative
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             AS CC CHEMOKINE RECEPTOR PROTEIN, ITS PRODUCTION AND USE
CC CHEMOKINE RECEPTOR PROTEIN, ITS PRODUCTION AND USE
PATENT: JP 1997227599-A 1 02-SEP-1997;
TAKEDA CHEM IND LTD
OS RATTUS TATLUS (rat)
PN JP 1997227599-A/1
PD 02-SEP-1997
PF 22-FEB-1996 JP 1996035192
PF 160DA SUSUMD, FUJISAMA TOMOYUKI
PC CO7K14/705,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00
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E13732
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1 (bases 1 to 1544)

Honda,S. and Fujisawa,T.

CC CHEMOKINE RECEPTOR PROTEIN, ITS PRODUCTION AND Patent: JP 1997227599-A 1 02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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JP 1997227599-A/1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diversity of free-living and attached bacteria in offshore western
Mediterranean waters as depicted by analysis of genes encoding 16S
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HONDA SUSUMU, FUJISAWA TOMOYUKI
C77K14/705,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,
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Location/Qualifiers
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327 c 447 g 324 t
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/isolate="SUR ATT"
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                             /product='Rat CC chemokine receptor protein' 1101. .1544.
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No. 8.17e+03
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Cyprinus carpio mRNA for MyoD, complete cds.
AB012882
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16S ribosomal RNA; ribosomal RNA small subunit C.trachomatis (strain 434) DNA.
Chlamydia trachomatis
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C.trachomatis 165 ribosomal RNA gene.
M59178
                                                                                                                                                                                                                                                                               Direct Submission
Submitted (09-APR-1998) to the DDBJ/EMBL/GenBank databases. Shugo
Watabe, The University of Tokyo, Graduate School of Agricultural
and Life Sciences; Yayoi 1-1-1, Bunkyo, Tokyo 113-8657, Japan
(E-mail:awatabe@hongo.ecc.u-tokyo.ac..p,
Tel:81-3-3812-2111(ex.7522), Fax:81-3-5684-0622)
                                                                                                                  Kobiyama, A., Nihei, Y., Hirayama, Y., Kikuchi, K., Suetake, H., Johnston, I.A. and Watabe, S.
Molecular cloning and developmental expression patterns of the MyoD and MEF2 families of muscle transcription factors in the carp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa: Chordata: Vertebrata: Actinopterygii: Neopterygii: Teleostei: Euteleostei: Ostariophysi: Cypriniformes: Cyprinoidea: Cyprinidae: Cypriniae: Cypri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyprinus carpio cDNA to mRNA Cyprinus carpio
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/organism="Rattus rattus"
/db_xref="taxon:10117"
a 347 c 330 g 452
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/db_xref="taxon:813"
324 c 472 g 358 t
                                                              Location/Qualifiers
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/organism="Cyprinus carpio"
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92947305
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Gant.T.M., Harris.C.A. and Wilson,K.L.
Roles of LAP2 proteins in nuclear assembly and DNA replication:
truncated LAP2 beta proteins alter lamina assembly, envelope
formation, nuclear size, and DNA replication efficiency in Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Cell Biol. 144 (6) (1999) In press 2 (bases 1 to 1563)
Gant, T. M. and Wilson, K.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-FEB-1998) Cell Biology and Anatomy, Johns Hopkins University School of Medicine, 725 N. Wolfe St., Baltimore, MD
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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           /translation="Mperiodpsyltkeklkselvannvtlpsgeorkdyrvolyloh
LTSONRATPDFSSDEEREAT PWRGGREPGRKATKKTDKPRAEEKDDPDTELSNEAL
KEELLKYGMKPGPILSNTRKLYEORLLKLESGGLESSAPBADSSKADNKONGNTDSEH
YSDKEEEAKIELTFEKREPLRGKSKTOVMRNRRTEKTETVSEDYVTEAAMVTSGPAKSG
PVOTVYKELAKVTRRTPRKKVVAPDPVPFDDADIAEVPPISESVVEPASNQILTYAEN
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IRLIDVHSIGFTNPTDLLKTALTETKHIIEDSLETPKKTOLKITKFVTPVKKQIVE
KTFEERRTERDILKEMFFTEFSTPTGISASCRRPIRGAAGRPLMATDLKINETYTSKY
VSNVSKYTPAVEYKSEKVKPGRSLPVMIKILMFLILVVFCLLVYQAMETNEGMSFSKL
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191. .1018
                                                                                                                                                                                                            /product="lamina associated protein
/protein_id="AACO5383.1"
/db_xref="pID:92947306"
/db_xref="GI:2947306"
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/db_xref="PID:g3721609"
/db_xref="GI:3721609"
                                                                                                                                                                                                                                                                                                                                                                    /clone="4"
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/db_xref="taxon:8355"
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Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Cyprininae;
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DRITGLSSTSSRLQYTARKEDVESQTTGTAKHYMGPDQVSEPEFPHYFTEKYSLQV
VSQSPIREGEDVTLKCQADGNPPTSFNFNIKGKKVTVTDKDFSFPHYFTEKYSLQV
VSQSPIREGEDVTLKCQADGNPPTSFNFNIKGKKVTVTDKDFSTFDTRADSGIYK
CSLLDNDVMESTQFTSLDYSLTPTGKVLKNVGENLIVSLDKNASSEKTVTWTKDN
RKLDKLPDFSKLTYSDAGLYVCDVSIEGIKRSLSFELTVEGIPKITSLTKHRSSDGKH
KVLTCEAEGSPKPDVQMSVNGTNDEVSYNNGKATYKLTVVPSKNLTVSCLVTNKLGED
TKEISVFSQKNEDGTEQAKVIVGIVVGLLVAAALVGLIYMIYIKKTRQGSWKTGEKEA
GTSEESKKLEENNHK"
363 c 400 g 328 t
                                                                                                                                                                                                                                                                                                                                     /function="putative cell adhesion molecule"
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/db_xref="61:407319"
/db_xref="61:407319"
/db_xref="61:407319"
/db_xref="61:407319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="retina, 14 d after optic nerve transsection"
<1. .>1569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
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M55916.1
                                                                                                                        Oryctolagus cuniculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Lagomorpha; Leporidae; Oryctolagus
1 (bases 1 to 1578)
201nlerowicz, S., Csortos, C., Bondor, J., Verin, A., Mumby, 1
 2 (bases 1 to 1578)
DePaoli-Roach, A.A.
                                                   DePaol1-Roach, A.A.

Diversity in the regulatory B-subunits of protein phosphatase 2A:
Identification of a novel isoform highly expressed in brain
Biochemistry 33, 11858-11867 (1994)
                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus protein phosphatase 2A1 B gamma subunit (skeletal muscle isolate) mRNA, complete cds.
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Isolation and heterologous expression of a cDNA encoding bovine insaltol polyphosphate 1-phosphatase proc. Natl. Acad. Sci. U.S.A. 87, 9548-9552 (1990)
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Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea;
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TVALLSKVLNGNKLASEALAKVVHQDVEFSDPALDSVEINIPODILGIWVDPIDSTYQ
YIKGSADITPNQGIFPSGLQCVTVLIGYYDIQTGVPLMGVINQPEVSQDLTHRRWKGA
CYWGLSYLGTNIHSLLPPVSTRSNSEAQSQGTQNPSSEGSCRFSVVISTSEKETIKGA
LSHVCGERIFRAAGAGYKSLCVILGLADIYIFSEDTTFKWDSCAAHAILRAMGGGMYD
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/protein id-"AAA30588.1"
/db_xref-"PID:g163223"
/db_xref-"01:163223"
/db_xref-"01:163223"
/translation-"MSDILQELLRYSEKAANIARACRQCETLFQLLIEEKKEGEKNKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/tissue_type="brain"
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Submitted (03-MAY-1994) Anna A. DePaoli-Roach, Biochemistry
Molecular Biology, Indiana University School of Medicine, 63
Barnhill Drive, Indianapolis, IN 46202, USA
                                                                                                                                                                                                                                       1 (bases 1 to 1614)
Hirschberg, J., Cunningham, F. Xavier Jr.
Lycopene cyclase gene
Patent: US 5792903-A 4 11-AUG-1998;
                                                                                                                                                                                                                                                                                                                                 Unknown
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GGRVVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLKSLEIEEKINKIKWLPQQN
AAHSLLSTNDKTIKLWKITERDKRPEGYNLKDEEGKLKDLSTVTSLQVFYLKPWLWV
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EDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDKHSKLFEEPEDPSNRSF
FSEIISSVSDVKFSHSGRYMLTRDYLTVKVWDLNMEARPIETYQVHDYLRSKLCSLYE
                                                                                                                                                                  /organism="unknown"
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/dev_stage="adult"
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/db_xref="taxon:9986"
/clone_lib="Lambda gt
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/protein_id="AAA58956.1"
/db_xref="ptD:9619215"
/db_xref="GI:619215"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2 from 101971
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Location/Qualifiers
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A32139
                                                                                                                                                                                                                         President and Fellows of Harvard College; Cambridge, MA
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Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 1658)

5 Shibata, D., Katto, T. and Ota, H.

5 Shibata, D., Katto, T. and Ota, H.

5 DNA CODING NEW CYTOCHROME P450

Patent: JP 199724671-A 1 02-SEP-1997;

PATENTIC GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK

OS GlyCine max (soybean)

PN JP 199724671-A/1

PD 02-SEP-1996 JP 1996031075

PF 19-FEB-1996 JP 1996031075

PF 19-FEB
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Glycine max
Glycine max
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4-hydroxybiphenol; UDP-glucuronosyltransferase.
Oryctolagus cuniculus (strain New Zealand White) adult liver
Oryctolagus cuniculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 1671)
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p 199724671-A/1
02-SEP-1997
19-FEB-1996 JP 1996031075
SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
C12N15/09,C12N9/02,(C12N9/02,C12R1:91);
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Dupuis-Williams,P., Klotz,C., Mazarguil,H. and Beisson,J.
The tubulin gene family of Paramecium: characterization and expression of the alphaPT1 and alphaPT2 genes which code for alpha-tubulins with unusual C-terminal amino acids, GLY and ALA Biol. Cell 87, 83-93 (1996)
2 (bases 1 to 1689)
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                                                                        Submitted (22-JUL-1996) P. Dupuis-Williams, Neurobiologie de la Diversite Cellulaire, ESPCI, 10 rue Vauquelin, F- 75005 PARIS,
                                                                                                                                                                                                                                                                                                    Paramecium tetraurella
Eukaryota; Alveolata; Ciliophora; Nassophorea; Peniculida;
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X99489.1 GI:1460089
alpha-tubulin; alphaPTl gene.
Paramecium tetraurelia.
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                                     Related sequence: Science 266:1688-1691 (1994).
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tetraurelia alphaPT1
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ONSQWXYFSLLOKLFSEXSDSCENACKEVVFNKTLMTKLQESKEDILLSDAIGBCGEL
LAELLKIPFVSLRFTPGVTNEKYSGGLSVPPSYVPIILSDLSGKMTEMERVNUNLCL
LXFDFWFOMFNKKRWDQFYSEVLGRPVTFSELVGKADMWLIRSYWDLEFPRPTLPNIO
LYFDFWFOMFNKKRWDQFYSEVLGRPVTFSELVGKADMWLIRSYWDLEFPRPTLPNIO
FVGGLHGKPAKFLPKENEEFVQSSGEEGVVVFSLGSMYSNMTEERANLIASAFAQLPQ
KVIMRFDGQKFETLGPWTRIVDWIFQNDLLGHKTKAFVTHGGANGIYEALHHGIPM
KVGLHGKPDGYKFETLGWTRIVDWIFQNDLCHKTKAFVTHGGANGIYEALHHGIPM
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/protein_id="AAA18021.1"
/db_xref="pID:gli55799"
/db_xref="GI:165799"
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Submitted (14-JUL-1997) Stetzer E., Institute of Physiological Chemistry, Johannes-Gutenberg university of Mainz, Duesbergweg
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Locusta migratoria
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Orthoptera; Caelifera; Acrididae; Oedipodinae; Locusta.
1 (bases 1 to 1698)
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/db_xref="07:1460090"
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/db_xref="taxon:5888"
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/db_xref="taxon:7004"
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226. .1575
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/codon_start=1
/product="nicotinic acetylcholine receptor, beta subunit".
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G-proptein coupled: link phospholipase C; serotonin receptor.
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Aplysia californica Ap5htBl gene, complete cds.
L43557
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LIITVAVVGNVLVCLAIFTEPILSHSKNEFIVSLAVADLLLALVMTFALVIMMYGY
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LMICSFYLSFVPIFLEWHELSVEEIKAIFKDNKTEKEKALEAHNFSSALNQTLGDNQK
SNAKHVCLFDVHFTYSVIYSFICFYVPCTLMLTMYLRLFILRPIABADEHLIPLECHE
OLRGOGASSYRRROGTOGSKAARTLIITIGTFLACWLFPFIINPIABADEHLIPLECHE
OLRGOGASSYRROGTOGSKAARTLIITIGTFLACWLFPFIINPIABADEHLIPLECHE
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252. .1613
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/db_xref="PID:g899118"
/db_xref="GI:899118"
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/db_xref="taxon:6500"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
euphyllophytes; Fabaceae; Papilionoideae; Arachis.
Rosidae; Fabales; Fabaceae; Papilionoideae; Arachis.
1 (bases 1 to 1704)
          Limulus polyphemus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata;
Xiphosura; Limulidae; Limulus.
1 (bases 1 to 1716)
Way,M., Sanders,M., Garcia,C., Sakai,J. and Matsudaira,P.
Sequence and domain organization of scruin, an actin-cros
protein in the acrosomal process of Limulus sperm
                                                                                                                                                             g558672
Z38129.1 GI:558672
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238129
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AAAIIIGSDPVPEVENPLFEIVSTDQQLVPNSHGAIGGLLREVGLTFYLNKSVPDIIS
QNINGALSKAFDPLGISDYNSIFWIAHLGGRAILDQVEQKVNLKPEKMKATRDVLSNY
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Maki, N., Watanabe, K. and Suzuki, M. PRODUCTION OF MATURATION PROTEIN USING CHIMPRODUCTION PROTEIN USING CHIMPRODUCTORY

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PF 19-JUN-1991 JP 1989154757
PF 19-JUN-1991 JP 1989154757
PF 19-JUN-1993 JP 1989154757
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J. Cell Biol. 128 (1-2), 51-60 (1995)
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31-JAN-1991
19-JUN-1989 JP 1989154755
MAKI NOBORU, WATANABE KAZUYA, SUZUKI MASANORI PC
MAKI NOBORU, WATANABE KAZUYA, SUZUKI MASANORI PC
21/02,C07K7/08,C07K13/00,C07K15/12,C12N1/19,C12N15/62,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="actin"
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ettfnsimkcovdirkolyantvlsggstmfpgiadrmqxeicalapstmkikilapp
etgrysvmiggilaslststydpmiskqeydesgpsivhrkcf"
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346 c
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/clone_lib="Limulus polyphemus
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/db_xref="taxon:6850"
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Pred. No. 8.17e+03;
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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              1548 TTCTGAGAA 1556
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OS Homo sapiens (Human)
PN JP 1991022984-A/2
PD 31-JAN-1991
PF 19-JUN-1989 JP 1989154758
PI 19-JUN-1989 JP 1989154758
PI MAKI NOBORU, WATANABE KAZUYA, SUZUKI MASANORI PC
C12N15/14,(C12N1/19,C12P21/02,(C12N1/19,C12R1:85),(C12P21/02, PC
C12R1:85);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=Liver;
CC *source: tissue_type=Liver;
CC *source: clone=Lumdagtl1(HSA-II);
FH Key Location/Qualifiers
FT CDS /product='Human serum albumin'.
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ttctgagaa
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1 (bases 1 to 1758)
Maki.N., Watanabe,K. and Suzuki.M..

PRODUCTION FOR HUMAN SERUM ALBUMIN A
PAtent: JP 1991022984-A 2 31-JAN-1991;
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*source: clone=put-HSA-CH;
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Location/Qualifiers
1. .1758
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/db_xref="taxon:32630"
348 c 406 g 458 t
                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
348 c 406 g 45
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1. .1758
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Pred. No. 8.17e+03;
0; Mismatches 0
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/product=' human serum albumin'
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c human serum albumin
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8.17e+03;
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E10761;
E10761.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Eukaryota; Metazoa; Ch
Catarrhini; Hominidae;
                                                                                                                                                                                                                                           1551 TTCTGAGAA 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent number JP 19
ASAHI GLASS CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Higashida H., Murakami K., Hama Y., Tsukamoto "MODIFIED GENE CODING HUMAN SERUM ALBUMEN"; Patent number JP 1996051982-A/3, 27-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variant cDNA encoding JP 1996051982-A/3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-1997 (Rel. 08-OCT-1997 (Rel.
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11-AUG-1994 JP 1994209369
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IP 1996051982-A/3
                                                                 g217534
D00361.1 GI:217534
cytochrome; cytochrome
Bovine adrenal cortex,
Artiodactyla; Ruminantia;
1 (bases 3 to 1786)
Morohashi,K., Yoshioka,H.,
                                                                                                                                         BOVCYPB 1786
Bovine cytochrome
                                                                                                                             D00361
                            Eukaryota; Metazoa; Chordata; Vertebrata; Martiodactyla; Ruminantia; Pecora; Bovoidea;
                                                          Bos taurus
                                                                                                                                                                                                                                                                   100.0%;
Similarity 100.0%;
9; Conservation
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                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
BP; 548 A; 351 C; 407 G; 455 T; 0 other:
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 Yoshioka, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="EcoRI recognition between second
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/clone_lib="human liver cDNA library"
/clone="pTL2Bmc"
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1129. .1134
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Last updated, Version
human serum albumin.
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P-450(11 beta)
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Pred. No. 8.17e+03;
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 Gotoh, O.,
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 Okada,Y.,
                                                                      clone pcP-450(11 beta)-3
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 Yamamoto, K.,
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                                           Eutheria;
                             Bovinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miyata,T., Sogawa,K., Fujii-Kuriyama,Y. and Omura,T.
Molecular cloning and nucleotide sequence of DNA of mitochondrial
cytochrome P-450(11 beta) of bovine adrenal cortex
Cytochem. 102 (3), 559-568 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning of cDNA encoding steroid 11 beta-hydroxylase (P450c11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chua, S.C
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                                                                                                                                                                                                                                                                                                                            /translation="MALWAKARVRMAGPWLSLHEARLLGTRGAVAPKAVLPFEAMPRC
PGNKWARMLQIWKEQGSENMHLDMHQTFQELGPIFRYDVGGRHWVFVMLPEDVERLQQ
ADSRHPQRMILEPWLAY RQARGKCGVFLLNGPQWRLDRLFLNPDVLSLPALQKYTPL
VDGVARDFSQTLKARVLQNARGSLTLDIAPSVFRYIEASTLVLYGGRLGLLTQQPNP
DSLNFIHALEAMLKSTVQLMFVPRRLSRWMSTNMWREHFEAWDYIFQYANRAIQRIYQ
ELALGHFWHYSGIVAELLMRADMTLDTIKARVHDTLTAGSVDTTAFPLLMTLFELARNP
EVQQAVRQESLVAEANISENPQRAITELPLLAALKETLALYPVGITLEREVSSDLVL
QNYHIPAGTLVKVLLYSLGRNPAVFARPESYHPQRWLDRGSGSRFFPHLAFGFGVRQC
LGRRVAEVEMLLLHHVLKNFLVETLEQEDIKMVYRFILMPSTLPLFTFRAIQ"
                            Biochem.
                                                                                                               Biochem.
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/db_xref="PID:d1000717"
/db_xref="PID:g217535"
/db_xref="GI:217535"
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/db_xref-"taxon:9913"
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102, 559-568 (1987)]; a in [2]"
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559-568 (1
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559-568 (1987)], [2]
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(1987)], [2]"
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 CLECOL2G 1790 bp DNA INV 31-DEC-19 C. elegans (nematode) collagen 2 (col-2) gene, complete cds.
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I50944.1
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Mason,J.M. and Squinto,S.P.
Retroviral vector particles expressing
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0; Mismatches 0
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/db_xref="taxon:6239"
prim_transcript 362. .1388
/note="col-2 mRNA (3' end approx)"
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Kramer,J.M., Cox,G.N. and Hirsh,D.
Expression of the Caenorhabditis elegans
col-2 is developmentally regulated
J. Biol. Chem. 260, 1945-1951 (1985)
85105075
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J155261 GI:156261
Collagen. DNA, clones lambda-CG[2,3,7,8,12] [1] and clones
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Draft entry and printed copy of sequence [2] were kindly provided by J.M.Kramer, (05-AUC-1985).
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Caenorhabditis elegans
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Rhabditidae; Caenorhabditis
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   GI:2169639
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/db_xref="PID:g156262"
/db_xref="GI:156262"
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/note="collagen"
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/note="collagen"
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PN JP 1987275695-A/1

PD 30-NOV-1987

PF 20-FEB-1987 JP 1987037683

PF 21-FEB-1986 FR 86 8602379

PI MARUTEIN RAIA, JIYAN FURANSOWA MAYOO, PAORO SARUMIENTOSU PC C12P21/02,C07K13/00,C12N15/00,(C12P21/02,C12R1:19); CC strandedness: Double; CC topology: Linear; CC topology: Linear; CC anti-sense: No; CC anti-sense: No; CC *source: tissue_type=liver; CC *source: clone=pXL53; FH Key Location/Qualifiers

FH CDS /product='mature type of human albumin' FT reat contide 1 1758
                                                                                                                  1 (bases 1 to 1797)
Dale,B. and Cordell,B.
Method and compositions useful in preventing eq
Patent: US 4920213-A 3 24-APR-1990;
Biotechnology Research Partners, Ltd.;
Mountain View, CA
On Jul 30, 1993 this sequence version replaced
Location/Qualifiers
ce 1, 1797
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1 (bases 1 to 1814)
Studler, J. M., Glowinski, J. and Levi-Strauss, M. Studler, J. M., Glowinski, J. and Levi-Strauss, M. an abundant mRNA of the embryonic brain persists at a high level in cerebellum, hippocampus and olfactory bulb during adulthood Eur. J. Neurosci. 5 (6), 614-623 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (29-JUN-1995) Jeanne-Marie Studler, INSERM U-114, College
de France, 11 Place Marcelin Berthelot, Paris cedex 05, 75231,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chicken.
Gallus gallus
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Studler, J.M.
                                             Homo sapiens
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imates; Catarrhini; Hominidae;
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/tissue_type="cerebellum"
63. .269
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/protein_id="AAA74902.1"
/db_xref="p11:963090"
/db_xref="p11:963090"
/translation="MIYQPRQTIWVSQKVFPTSQGDGGFLKGCLPISKEVNRKKESEV
EGACWAPVNGDGHHFTKINYLYTF"
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1814
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349 c 347 g 60
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/Ah vrof="tavon:903]"
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                 Vertebrata; Mammalia; Eutheria; ae; Homo.
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Matches 9; Conservative
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ttctgagaa 33
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Segre, G.V., Kronenberg, H.M., Abou-Samra, A., Juppner, H., Potts, J.T.
Jr. and Schipani, E.
DNA and vectors encoding the parathyroid hormone receptor,
DNA and vectors encoding the parathyroid hormone receptor,
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PATENT: WO 9523857-A 1 08-SEP-1995;
DELTA BIOTECHNOLOGY LTD (GB)
Other publication AU 1818395 950918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2 from patent US 5494806. I17765
                                                                                                                                                                                                                                                                                                                                                                                   Unknown
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Location/Qualifiers
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evtepaktcvahesaencdksihtlegdkictyatlretygebadecakqeepernece
lqkeddnpnlprlyrpedvygctafhdneetelkkylyeialarheysgapeellefakr
ykaafteccqaadkaacllpki.delrddegkasakqrlkcaslqkegerafkawavar
lsqrfpkaefaevsklytdltkvhtecchgdllecaddradlakyicenqdsissklk
eccekpllekshciaevendewpadlpslaadbyeskovgkkyraekbyflgweybel
eccekpllekshciaevendewpadlpslaadbyeskovgkkyraekbyflgweybel
arrhedysvylllakakyettlekcaaadbyeskovgkkyraekbyflgweybel
elfeqlgeykfqnallyrytkytgytlvgysrnlgkygskckhpeakkwpcae
bylsyvlnglcylhektpysdrytkcteslvnrrpcfsaleydetyppkefraaetft
bylsyvlnglcylhektpysdrytkcteslvnrrpcfsaleydetyppkefraaetft
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CFAEEGKKLVAASQAALGL"
                                                                                                                                                             /organism="unknown"
495 c 522 g
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/db_xref="taxon:9606"
73. .1827
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conflict with the conceptual translation"
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/db_xref="PID:e306153"
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RESULT 102

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SFACT15B 1876) Strongylocentrotus X03076

franciscanus actin gene Sfa 15B.

25-MAR-1993

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Kalmokoff,M.L.,
and Teather,R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agriculture and Agri-Food Car
Ottawa, ON KIA 0C6, Canada
Location/Qualifiers
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Eubacteria; Firmicutes; Low G+C gram-positive bacteria;
Clostridiaceae; Butyrivibrio.
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AF026812
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GLSISEKMKKOIRGLGQASTANASDGVSSYQTAEGALTEVHDMLORMNELAVQAANGTN
SESDRSDIQNEIDQLTQGLIDRIASTTKENETEFILKGDVGLRHWYINAHDAGLDGTLIQ
NTTRATFTMESSLEAGERYTIGGTQYTIGASTNOEVAEALHLTQYYTAGATPTAAGTWK
LTAGDTISIDGKTYTINADDGTDIABAKUTNGYLAKLITKGSTYKYNGCEVTRESTS
LYAGGTISIDGKTYTINADDGTDIABAKUTNGYGLAKLITKGSTONAULTNYKYGCEVTRESTS
                                                                                                                                                                                                                                                                     YNSSTGIDDANVTLIKATAAYKMVAIXLKAASSIGATHGPASMDTAKTTSADGKVKAG
DYIWEKHNIKKTVDGKEITSTTYSFSITKGFVNIQNALTLNLHVGADAAMTNKINVTL
EAMNAKSIGIAGINVSDATGKNATYAIDAITDAIQRVSAQRAELGAVQNRLEHSIKNL
                                                                                                                                                                                                                                                      <u>DNVVRNTEAAESRIRDTDMADTMVEYSKNNILQQAGQSMLAQANQANQATQGVLQLLQ</u>
                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAB82613.1"
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/db_xref="GI:2583088"
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/strain="OR77"
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'gene="flaB"
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fibrisolvens strain OR77 flagellin B protein (flaB)
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I50943.1
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1 (bases 1 to 1980)
Mason.J.M. and Squinto,S.P.
Retroviral vector particles expressing
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I50943
                                                                                                                                                                                                                                                             Unknown
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Eubacteria; Firmicutes; Clostridium group firmicutes;
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/protein_id="AAC32611.1"
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/db_xref="taxon:1594"
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1 (bases 1 to 1980)
Einvik, C., Decatur, W.A., Embley, T.M., Vogt, V.M. and Johansen, S. Naegleria nucleolar introns contain two group I ribozymes with different functions in RNA splicing and processing
                                                                                                                                                             Submitted (27-NOV-1996) Zoology, Natural History Museum, Cromwell Road, London SW7 5BD, UK
                                                                                                                                                                                                                                                 Einvik,C., Decatur,W.A., Embley,T.M., Vogt,V.M. and Johansen,S. Naegleria nucleolar introns contain two group I ribozymes with different functions in RNA splicing and processing
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Embley, T.M and Dyal, P.L.
Direct Submission
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Naegleria jamiesoni
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Schizopyrenida; Vahlkampfiidae; Naegleria.
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                                                                      /db_xref="taxon:5764"
<1. .>1984
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                                           /product="18S
416 c 5
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/strain="T56E"
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/strain="PPMFB-6"
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On Jul 30, 1996 this sequence version replaced g1:695508
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3 (bases 1 to 1992)
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Medicine, Center for Vaccine I
Baltimore, MD, USA, 21201
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A plasmid-encoded regulatory region activates chromosomal eaeA expression in enteropathogenic Escherichia coli infect. Immun. 63 (5), 1767-1776 (1995)
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CYVKKXIFTANLNEMOLNIVSNIITDIKYSGNNKKIFKILYLLSFFNDYNDIVBVILS
ASSKSIVDRVIKVIELDISKNWKLGDVSSSNFMSDSCLRKQLNKENLTFKKIMLDIKM
                                                                                               KHASLFLRTTDKNIDEISCLVGFNSTSYFIKVFKEYYNTTPKKYNGVYSITQGTLP"
                                                                                                                                                                                                                                                                                                                                                                        transcription. Belongs /citation=[1]
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transcription. Belongs to the AraC family"
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Local Similarity 100.0%;
hes 9; Conservative
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                                                                                            g1098626
U31079.1
Danio rerio
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                Danio rerio
                                                             zebrafish.
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VTKLDNKAAHCHSPVLQRHRPFLGRRLDCQPHRR"
302 c 352 g 571 t
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SYASNVIKFIITMEGGGDILSESKRAP"
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transcription"
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                                                                                                GI:1098626
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="CAA88448.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="fourth ORF of four ORFs that together increase eaeA
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RFCINKSLRNNLQADNYSDIKQGVYKAYKKMGLVNEKIFRNYKEN"
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/transl_table=11
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/gene="perC"
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/note="third_ORF of four ORFs that together increase eaeA
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1367, .1636
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[367. 1636
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1342. .1347
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47 kDa heat
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Pred. No.
0; Misma
                                                                                                                                              mRNA VRT
shock protein (hsp)
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d. No. 8.17e+03;
Mismatches 0;
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Pearson, D. S., Kulyk, W.M., Kelly, G.M. and Krone, P.H. Cloning and characterization of a cDNA encoding the collagen-binding stress protein hsp47 in zebrafish DNA Cell Biol. 15 (3), 263-272 (1996)
96226405
                                                                                                                                                                                                                          Sequence
I04790
                                          Cloned human serum albumin gene
Patent: EP 0206733-A1 3 30-DEC-1986;
Location/Qualifiers
1. 2015
                                                                                                     Burns, A.L.
                                                                                                                                                                                                         g591462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-JUL-1995) Patrick Krone, Anatomy and Cell Biology, University of Saskatchewan, Health Science Building, 107 Wiggins Road, Saskatoon, Saskatchewan S7N 5E5, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pearson, D.S., Kulyk, W.M. Direct Submission
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snyfhasslehdtegnfedpsifgsekmrnpklfyadhpfiflykdnktnsilfigrl
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1377. .1399
/note="encodes RDEL endoplasmic
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178. .1392
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178. .1392
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406 c 447 g
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Gallus gallus j
(crds1) mRNA,
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Eukaryotae; Metazoa; Chordata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallu
1 (bases 1 to 2046)
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A40251.1
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A40251
                                                                                    2 (bases 1 to 2046)
Weng, J. and Travis, G.H.
Direct Submission
Submitted (23-OCT-1997) Psychiatry, UT
5323 Harry Hines Boulevard, Dallas, TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unidentified
                                                                                                                                                                             Weng, J., Belecky-Adams, T., Adler, R. and Travis, G.H. Identification of two rds/peripherin homologs in the chick retina Invest. Ophthalmol. Vis. Sci. 39 (2), 440-443 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marcussen, J.
TRANSGENIC ORGANISM
Patent: WO 9424292-A 1 27-OCT-1994;
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AF031238.1
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Similarity 100.0%;
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                                                              1. .2046
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557 c 552 g 43
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L. .2046
                                                                       ocation/Qualifiers
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                                                                                        Southwestern Medical Center, 75235-9111, USA
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Matches 9; Conservative
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U03906
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Macroscelidea; Macroscelididae;
                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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J. Biol. Chem. 271 (26),
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raham,C., Hodin,J. and Wistow,G.
retinalehyde dehydrogenase as a structural protein immedian eye lens. Gene recruitment of eta-crystallin cham. 271 (26), 15623-15628 (1996)
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/protein_id="AAC06274.1"
/db_xref="plb:92642234"
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ALCFFENILLFFVALICFLMRGSLESTLAQGLKNSMKFYRDTDTPGRCFMKKTIDDSLQ
IEFKCCGNNGFRDWFESLQWISNRYLDFSSKEVKDRIKSNVDGRYLVDGYPFSCCNPSS
PRPCIQYQVTNNSAHYSYDYQTEELNLWGRGCREALLHYYSSMMSSNGAVVLLVWLFE
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GAEGAEGEEAGKTPAITTVS"
GVCGQIFPWNAPMILLACKIGPALCCGNTVIVKPAEQTPLTALHVASLIKEAGFPPGV
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/db_xref="taxon:29082"
/tissue_type="lens"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="photoreceptor outer segment membrane
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272. .1336
                                                                                                 /evidence=experimental
/product="aldehyde dehydrogenase
/protein_id="AAC48588.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to mammalian rds/peripherin"
/codon_start=1
                                                                                                                                                                                          /EC_number="1.2.1.3"
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hesda, MD 20892 USA
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d. No. 8.17e+03;
Mismatches 0;
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RESULT 118
E11452
Standard; RNA; PLN; 2053 BP.
AC E11452.1
NI d1109789
DT 07-CCT-1997 (Rel. 52, Created)
DT 07-CCT-1997 (Rel. 52, Last updated, Version 1)
CC 08 Arabidopsis thaliana
PN JP 1996140686-A/5, 04-JUN-1996.
RL TOYOTA MOTOR CORP.
CC 08 Arabidopsis thaliana
CC PF 25-MOV-1994 JP 19964315514
CC PF 25-MOV-1994 JP 1994315514
CC PF ASADA CHIAA, OOTO TOKU, YAMAMOTO MASAYUKI, CC PI ASADA CHIAA, OOTO TOKU, YAMAMOTO 
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ORIGIN
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T "GENE CODING FOR VEGETABLE PROTEIN";

Patent number JP 1996140686-A/5, 04-JUN-1996.

L TOYOTA MOTOR CORP.

C SA Arabidopsis thaliana

PN JP 1996140686-A/5

C PD 04-JUN-1996

C PI 25-NOV-1994 JP 1994315514

C PI ASADA CHIKA, OOTO TOKU, YAMAMOTO MASAYUKI, SHIMODA PI ASADA CHIKA, OOTO TOKU, YAMAMOTO MASAYUKI, SHIMODA CORTISOPO, AOHSS: Double;

C C C12x15/99, AOHS/00, C07H21/04, C07K14/415, C12x15/10;

C C C12x15/99, AOHS/00, C07H21/04, C07K14/415, C12x15/10;

C C C topology: Linear;

C C C hypothetical: NO;

C C antisense: NO;

C C antisense: NO;

C FH Key

FT SOurce

/Organism-"Arabidopsis thaliana"

C FT CDS

/product-"plant protein which induce and spore

FT CDS

/product-"plant protein which induce and spore

formaticus."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosi
                                                    1018 TTCTGAGAA 1026
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ASADA CHIKA, OOTO TOKU, YAMAMOTO MASAYUKI, SHIMOD HIRAYAMA TAKASHI
C12N15/09,A01H5/00,C07H21/04,C07K14/415,C12N5/10;
strandedness: Double;
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IVFADADLDSAVEFAHOGVETINGGGSCIAASKLFVEETITYDERVGRSVERAKKYVFGN
PLTPGVHHGPQINKAGHNKIMELIESGKKEGAKLECGGFBWGNKGYFIOPTIFSNVTD
DMRIAKBEIFGPVQQIMKKFKSLDEVIKRANNTYYGLVAGVFTKDLDKAVTVSSALQAG
TYWVNCYLAASAQSPAGGFKMSGHGRENGEYGIHEYTEVKTVTMKISEKNS"

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                                                                                                              Pred.
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8.17e+03;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans U20902
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Submitted (07-DEC-1998) Protein Metabolism,
Institute, Greenburn Road, Bucksburn, Aberde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newbold, C.J.
Heat shock 70 protein
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1 (bases 1 to 2083)
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Kreutzer,M.A.,
Knoblich,J.A.,
                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabdito Rhabditidae; Caenorhabditis.

[ (bases 1 to 2090)
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Eschenlauer, S.C.P.,
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2 (bases 1
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/db_xref="taxon:47911"
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SKDDIDRLVKEAEKFKDEDNKVKERIESKNTLEQYCYQVRQTLTDEKLKDKFSEDEKK
QVGDKYDEVLKMVNDNPAASKEEYDAKYKEIEAVFNPIMQKIYQQMGGQPGGMPNFGG
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QATVDLDALMIGEDLNVVITRSKFEDLCVGLFRKCMFPLENVLKUAKMSKSQIDEVVL
VGGSTRIPKIQSMYQEFFIGKEPRKSINDEBANAYGAAVQAALMTNVKDENIEKLILL
DVTPLSLGIETVGGVMTVLIPRNSTIPCKKTQIFSTYSDNQPSVLVQVYEGERQLIKD
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/protein_id="AADJ7197.1"
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/db_xref="GI:4324942"
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/db_xref="GI:4324942"
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Richards, J.P., De Silva-Udawatta, M.N., Lehner, C.F. and Bennett, K.L.
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                        Temenak, J.J.,
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Eukaryotae; I
Vertebrata;
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Andrews J.B. and Holland, M.K.
The nucleic acid sequence of rabbit PH-20 cDNA Unpublished (1996)
                                                                                                                                                                                                                                 Direct Submission
Submitted (22-APR-1994) Jason B. Andrews, Division of Wildlife Ecology, CSIRO, PO Box 84, Lyneham, ACT 2615, Australia On Feb 23, 1996 this sequence version replaced gi:483923.
Location/Qualifiers
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/db_xref="product="cycling"
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/clone_lib="testis cDNA Holland"
                                                                         /clone="C"
                                                                                                                /organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
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Best Local Similarity 100.0%;
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I (bases 1 to 2113)

Spikes,D.A., Kramer,J., Bingham,P.M. and Van Doren,K.

Spikes,D.A., Kramer,J., Bingham,P.M. and Van Doren,K.

SWAP pre-mRNA splicing regulators are a novel, ancient protein family sharing a highly conserved sequence motif with the prp21 family of constitutive splicing proteins

Nucleic Acids Res. 22 (21), 4510-4519 (1994)
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                                                                                                                                                                                                                                                                                                                               Submitted (04-MAY-1994) Paul M. Bingham, State University of New York at Stony Brook, Life Science Bldg., Rm 450, Stony Brook, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae: Caenorhabditis.
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U09415.1 GI:498845
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                                                                                                                                        /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone_lib="Caenorhabditis elegans cDNA library, Waterson R., Nature Genetics 1:114-123(1992)"
15. .1982
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DPHTGAIVHGRIPQLGPLQQHLTKLRQBILYYMPKDNYGLAVLDMESWLFWLENWKP
KDIYRIKSIELVKSQHPQYNHSYATEKAKRDFEKAGKDFWEETLKLGRLLRPHLLWGY
YLFPDCYNHHYDKPNLYKGSCFDIEKKRNDDLSWLWKSSTALEFSVYLTSRARSATAL
SKLYVVRNRVHEAIRVSKIPDDKSPLPNFVYTRLVFTDQIFQFLSHHDLVYTIGEIVA
LGASGIYVWGSQSLARSWKSCLHLDNYKKTILMPYLINVTLARKCNQVLCQEGGVCT
RKNWRNDYLHLNPGWFAIQLGSWGTTYMDGKTTTDLDEGTSNNFQCSCYTNLWKCER
RKNWRNDYLHLNPGWFAIQLGSWGTTWTDAFKEKDVAHILSNTTSINSSTTMSLPF
PRKHVSGCLLVLCMYSQYLNICYRLVAIGIQHGYYLK"
                      /gene="Ceprp21"
/standard_name="Caenorhabditis elegans pre-RNA processing
21"
                                                                                              /gene=
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/product="PH-20 protein"
/protein_id="AAA88913.1"
/db_xref="pID:g1199859"
/db_xref="GI:1199859"
/translation="MGVLKFKHIFFGSAVELSGVFQIVFIFLLIPCCLTANFRAPPVI
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393 c 435 g 639
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/tissue_type="testis"
/note="similar to yeast pre-mRNA splicing factor PRP21,
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                              ne="Ceprp21"
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Pred. No. 8.17e+03;
0; Mismatches 0;
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hes 9; Conservation
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                                                                                                                                                                       Worman,H.J.

Direct Submission

Direct Submission

Submitted (03-UUL-1990) H.J. Worman, THE ROCKEFELLER UNIVERSITY,

SUBMITTED FOR AVENUE, NEW YORK NY 10021, USA

2 (bases 1 to 2123)

Worman,H.J., Evans,C.D. and Blobel,G.

The lamin B receptor of the nuclear envelope inner membrane: a

polytopic protein with eight potential transmembrane domains

J. Cell Biol. 111 (4), 1535-1542 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus
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Chicken mRNA for lamin
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 2123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lamin B receptor.
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/dev_stage="embryo"
/clone_lib="lambda zap"
1. 2123
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/note="encodes surp module 1"
414. .542
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VLALGADISRNLGREAERRTDIFGVGGEQTMIGKKIGGEEDNSQOGQNKLIWDGTEETR
DMITRAVQNKYTLDQOINEIHROHIGFVADPSKEKIGAGENFAUSTGQUIPTITOGITN
IPGQMPSGWPPVPPMGMPGMENQALPPIRQMDFGGGEPAKRPRTEDDLIPTITOGITN
VNGAISLNYHLPQAPEHGMDGSIVQFTIQVTAPMSELKQQIQDRYGMPVGKQKLMSDGL
FYKDNMSSAFYNLADRTAIYLQVKERGGKKK"
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/db_xref="PID:9498846"
/db_xref="GI:498846"
/db_xref="GI:498846"
/ta_nslation="MTAVVSNREEDSMNNEPSLSGRAIIGLIYPPPDIRTIVDKTARF
/ta_nslation="MTAVVSNREEDSMNNEPSLSGRAIIGLIYPPPDIRTIVDKTARF
AAKNGVDFENKIREKEAKNPKFNFLSITDPYHAYYKKMVYDFSEGRVEAPKVPQAVKE
HYKKAEFYPSAPPPAYEFSADPSTINAYDLDLIRLVALFVARNGRQFLTQLMTREARN
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KHQKGLKDREEAEAEKERQAYASIDWHDFVVVQTVDFQPGDTSQLPPLCTPKDVGARI
LLEARNEMOKAAAEMQEMDWEESDSDDEDAVQAPEAPAFTAPLPPTKQKDVIVRDYDP
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/gene="Ceprp21"
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/note="encodes surp
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489 g
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Pred. No. 8.17e+03;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                      VCAM variant
A30921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenBank staff at the National Library of Medicine created entry (NCBI gibbsq 163794) from the original journal artice. This sequence comes from Fig. 1A.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S76880 2202 bp
XIdx=bHLH function de
                                                    Patent:
                                                                                                         artificial
                                                                                                                    synthetic construct.
synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Plpidae; Xenopodinae; Xenopus.

1 (bases 1 to 2202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S76880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mech. Dev. 49 (
                                                 PHARMACEUTICAL COMPOSITION COMPRISING A CELL ADHESION MOLECULE atent: WO 9200751-A 11 23-JAN-1992;
                                                                                           (bases 1 to 2220)
                                                                                                                                                                                                                                                                                                                                                                                                  617
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                                                                                                                                                                                                                                                                                                                                                                                               SDFSELATQGDTSVCH"
485 c 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"bHLH function dominant sequence comes from Fig. 1A"
                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKAISPVRSMSSCYQAVCCLSEQSLSIARGSSHKGPGMDEPMGL
/translation="MKAISPVRSMSSCYQAVCCLSEQSLSIARGSSHKGPGMDEPMGL
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/db_xref="taxon:32630"
                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="XIdx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                                                                                                                            GI:1247240
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"GI:914115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAB34225.1"
/db_xref="PID:g914115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product-"XIdx"
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                                                                                                                                                                                                                                                                                                                            Score 9;
Pred. No.
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patent W09200751.
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8.17e+03;
-hes 0;
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                        misc_feature
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
1 (bases 1 to 2223)
1 (Bases 2 to 2223)
1 (Bases 2 to 2223)
1 (Bases 3 to 2223)
1 (Bases 4 to 2223)
1 (Bases 5 to 2223)
1 (Bases 5 to 2223)
1 (Bases 6 to 2223)
1 (Bases 7 to 2223)
1 (Bases 8 to 2223)
2 (Bas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-OCT-1997) Dental 601 Elmwood Ave, Rochester, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hagen, F.K. and Ne
Direct Submission
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/product="GLY5b"
/product="GLY5b"
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IVKKGDAAQAGELGKAVVVDKKLSTEEKAKYDKGMLNNAFNQYXSDMISVHRTLFTN
IDAECKTEKYNENLPRTSVIIGFHNEAWSVLLRTVHSVLERTPDHLLEEVVLVDDFSD
MDBTKRPLEEYMSQFGGKVKLIRMEKREGLIRALKGAAVATGEVLTYLDSHCECKEG
WMEPLLDRIKRDPTTVVCPVIDVIDDNTFEYHHSKAYFTSVGGFDWGLQFNWHSIPER
DRXNRTRPIDPVRSSTMAGGLFSIDKEYFEKLGTYDDGFDIWGCSDLELSFKIMMCGG
TLEIVPCSHVGHVFRKRSPYKWRTGVNVLKRNSIRLAEVWLDDYKTYYYERINNQLGD
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1556. .1659
/gene="gly-5"
/note="GLY5b variant segment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /EC_number="2.4.1.41"
/note="UDP-GalNAc:polypeptide
N-acetylgalactosaminyltransferase splice variant 5b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="gly-5"
83. .1963
                                                                                                                                                                            RYNHDTGRLQHAVSQKCLGMTKDGAKLEMVACQYDDPYQHWKFKEYNEAKAIEHGAKF
                                                                                                                                                                                                                    FGDISSRKKLREDLGCKSFKWYLDNIYPELFVPGESVAKGEVRNSAVQPARCLDCMVG
RHEKNRPVGTYQCHGQGGNQYWMLSKDGEIRRDESCVDYAGSDVMVFPCHGMKGNQEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:6239"
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14642, USA
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Matches
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Best Local Similarity 100.0%;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                     25 ttctgagaa
                                           33 ttctcagaa
                                                                                                                                                                                                                                                                                            Sequence 3
109216
9588076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moos,M. Jr., Krinks,M. and Wang,S.
Production and use of anti-dorsalizing morphogenetic Patent: US 5693779-A 7 02-DEC-1997;
Location/Qualifiers
1. .2225
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Caras, I.W.
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Moos, M. Jr., Krinks,
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Best Local Similarity 100.0%;
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Rickettsia tsutsugamushi (strain Kawasaki) DNA.
Rickettsia tsutsugamushi
Rickettsia tsutsugamushi
Rickettsia; Proteobacteria; alpha subdivision;
Eubacteria; Proteobacteria; Rickettsia.
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450. .
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297 c 486
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79. .2126
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79. .84
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855 c 582 g 551 t
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19. .24
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus. 1 (bases 1 to 2400) Maeda, N., Ebert, D.L., Doers, T.M., Newman, M., Hasler-Rapacz, J., Attie, A.D., Rapacz, J. and Smithies, O. Molecular genetics of the apolipoprotein B gene in pigs in relation to atherosclerosis Gene 70 (2), 213-229 (1988)
                                                                                      1899. .2136
/gene="apoB"
/number=13
2137. .2400
/gene="apoB"
/number=14
a 577 c
                                                                                                                                                                                                           1638. .1898
/gene="apoB"
/number=13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="apoB"
185. .302
/gene="apoB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="YHRTNPTGTQDLLEIADYLLEQIRDNCTGNEDHTYLSLRVIGNI
GRTWEDLTPKLTSSYLKCIKSTQPPLLIQKAAIQASRKVELGDQVREVLLQTFLDNVS
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KKLVEEALKNSQLPTINDFKKFSRNYHFSKSISLPSLDPVSTTIEGNLIFDPNNYLPK
KKLVETALKNSQLPTINDFKKFSRNYHFSKSISLPSLDPVSTTIEGNLIFDPNNYLPK
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join(185. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="apolipoprotein
/protein_id="AAA64249.1"
/db_xref="PID:9727172"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sus scrofa"
/db_xref="taxon:9823"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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'number=13
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number=12
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                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="apoB"
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                    Score
Pred.
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     Mismatches
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                    8 9;
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                  DB 23; L
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                                    Length 2400
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                                                                                          15 others
     Indels
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   Gaps
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REFERENCE
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                                                                                                                                                                                                                                 Direct Submission submitted (05-AUG-1998) IGM, CNRS, route de Mende, Montpellier Cedex 5 34293, France
                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus
Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Ave
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 2409)
                                                                                                                                                                                                                                                                                                         receptor gene cluster
Genome Res. (1999) In press
2 (bases 1 to 2425)
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1 (Dases 1 to 2425)

Reboul, J., Gardiner, K., Monneron, D., Uze, G. and Lutfalla, G.

Reboul, J., Gardiner, K., Monneron, D., Uze, G. and Lutfalla, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chicken.
                                                                                                                                                                                                                                                                                               Reboul, J., Gardiner, K., Uze, G. and Lutfalla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="medlcvantlfalnlfkhlakasptqnlflspwsisstmamvym gsrgstedomakvlgrnevganavtpwtpentfscgfwqoiqkgstdaldkgrgadadk inastrulgrnevganavtpwtpentfscgfwqoiqkgstdaldkgrgadadk inastrulgrnevgrksfrevgryftrlcokyyssepqavdffle caearkkinswyktgrkipkllpbgsvdgdtrmvlvnavyfkgkwktpfekklng lypfrvnsaqrtpvqmmylreklnigyiedlkaqilelpyagdvsmflllpdeiadvs tglelleseitydklnkwtskokmaedbyevyipqfklehyelrsilasmgwedafn kgranfsgmsendlfflseyfhqamvdvneegteaaagtggvmtgrtghggpqfvadh pflflinkitkotlffsgressp p 658 t
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                                                                         76. .1785
                                                                                                                                              /organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="PID:g512778"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="protein with miniactivin activity"
/protein_id="CAA01261.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="synthetic construct"
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                                                                                                                                                                                                                        ocation/Qualifiers
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No. 8.17e+03;
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BASE COUNT
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ID. E11595;

AC E11595;

SV E11595,1

II d1109932

DT 08-OCT-1997 (Rel. 52, Created)

DT 08-OCT-1997 (Rel. 52, Last updated, Version 1)

DT 08-OCT-1997 (Rel. 52, Last updated, Version 1)
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 Query Match
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                                                                                                                         Shimada K., Takahashi M., Iijima Y., Tanzawa "HUMAN ENDOCELIN CONVERTING ENZYME"; Patent number JP 1996173154-A/1, 09-JUL-1996. SANKYO CO LTD.
                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
Sequence 2440 BP; 581 A; 736 C; 673 G; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1339 TTCTCAGAA 1347
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                                                                                                 source
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Catarrhini; Hominidae; Homo.
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JP 1996173154-A/1
09-JUL-1996
                                                                                                                                                       CDS
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SHIMADA KOHEI, TAKAHASHI MASAAKI,
TANZAWA KAZUHIKO
                                                                                                                                                                                              source
                                                                                                                                                                                                                                                   (C12P21/02,C12R1:19),(C12P21/02,C12R1:19);
strandedness: Double;
                                                                                                                                                                                                                                                                                A61K49/00
                                                                                                                                                                                                                                      topology:
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Similarity 100.0%;
9; Conservative
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Similarity 100.0%;
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                                                                                                                                                                                                                                      Linear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dl_xref="gi:4028135"
/translation="martacasgrlaavllcylvvsrccasgrinksppoliovyavn
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TNETLMMNYTGDGTNVTFSAQYGCFDDLQTSEPEWKELSGCQNVSHTECDFSSÄITAY
TYDTHIRIRAERREAKSPWSSIFEMIFYEIAQIGFPEIALQSINGAIKINISPPEANQ
YRXMMLISVFFKKINVLIWDNSSNVEKVRSILFIDVINLAPETTYCLKVQATVPLEDK
GGLFSPIHCIKTTRKVNDLLCPTNVRVFALNWKFYLLWDHYNEHVTTYVQTLTGYLK
KILIDDYSSKYGKYGGCENITSWKCHLSSVIKFTSASYYFRVQANNEYSKSCLEKDVEV
DPPVTNEIGFDDVKVDISDVLLHIKITPPGGPONKINSONEE
EVKMKETKOTIATVSDLAPSTLYCVKVQAFSEAYNKSSDFSREECIGTAGGKHLPLII
LAFFAGALTVVLIVASLVIFFLYQVYNKIKYMFFPSCOTFLNIEGFGAGLFSSFFVPT
TEEPVEICYIIESRITEEVNQIDFKDNKHFKQSSRDSGNYSYDDNTSQSKGSBETLGN
                                                                                                                         /product="endothelin-converting enzyme"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAD13669.1"
/db_xref="PID:g4028135"
                                                                                                 .2440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491
                                                                                                                                                      /organism="Homo sapiens"
/cell_type="umbilical vein endothelial cell"
62. .2338
                                                                                                                                                                                                                         Location/Qualifiers
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Score 9; DB 11; L
Pred. No. 8.17e+03;
0; Mismatches 0
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Pred. No. 8.17e+03;
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                                                          450 T; 0 other;
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                            Length 2440;
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 Indels
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Gaps

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RESULT 143
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Best Local Similarity 100.0%;
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                                                          N Sus scrofa vascular ce. 108351 g474382 U08351.1 GI:47430
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AF077838
g3414962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus. 1 (bases 1 to 2466)
Takamori,Y. and Inoue,A.
Dynamic properties of nuclear lamins in Xenopus cells
pig.
Sus scrofa
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-JUL-1998) Department of Biology, Graduate School of Science, Osaka University, Machikaneyama-cho 1-1, Toyonaka, Osaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2466)
Takamori,Y. and Inoue,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         African clawed frog. Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF077838.1
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506 c 634 g
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/protein_id="AAC31543.1"
/protein_id="PDI:93414963"
/db_xref="GI:3414963"
/translation="MATATPSGPRSSGRRSSMSTPLSPTRISRLQEKSDLQELNDRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nuclear lamina; located
inner nuclear membrane*
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/db_xref="taxon:8355"
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191. .1945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="intermediate filament protein; component of the
nuclear lamina; located on the nucleoplasmic side of tl
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                                                                                                                              cell adhesion molecule
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Pred. No. 8.17e+03;
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Tsang,Y.T., Haskard,D.O. and Robinson,M.K.
Cloning and expression kinetics of porcine vascular cell adhesion
1 (bases 1 to 2500)
Wang, E.A., Wozney, J.M. and Rosen, V.A.
NOVEL OSTEOINDUCTIVE COMPOSITIONS
                                                                                                                                                         Sequence 30
108629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-APR-1994) Yvonne T. M. Tsang, Pediatrics (Leukocyte Biology Section), Baylor College of Medicine, Texas Children's Hospital, Clinical Care Center, Suite 1130, 6621 Fannin, Houston, TX 77030-2399, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsang, Y.T.M.
Direct Submission
                                                                     Unknown
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                                                   Unclassified.
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Similarity 100.0%;
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/note="cytoplasmic tail"
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/cell_type-"endothelial cell"
/tissue_type-"aorta"
98. .19
98. .1714
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170. .1585
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LIIQAAPKDLQLTAFPSESVKEGDTVIISCTCGNVPPTLIILKKKAETGDTVLKSTDG
AYTIHRARLADAGVYECESKNEIGLQLRSITLDVKGRESNKDYFSSELLVLYCASSLI
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ISPKDPVISVNPSTSLQEGDSMMMTCTSEGLPAPQISWSKKLDNGDQQLLSGNATLTL
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LTCSAPDCESSLSFSWRTQIDSPLNGKVKTNGTRSTLVMNPVSFENEHSYLCTVSCGN
LKGERGIQVEIYSFPKDPEIHWSSLPEVGKPVTVRCLVPDVYPVEKLEIELLKDNHSM
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/product="vascular cell adhesion molecule"
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/db_xref="pip:9474383"
/db_xref="GI:474383"
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/db_xref="taxon:9823"
/clone="pV5"
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Local Similarity 100.0%;
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                                                                                                                                          Lactococcus lactis
Eubacteria; Firmicutes; Low G+C gram-positive bacteria;
Streptcoccaceae; Lactococcus.

1 (bases 1 to 2599)
Mierau, I., Tan, P. S.T., Haandrikman, A.J., Leenhouts, K.J., Kok, J.,
Konings, W.N. and Venema, G.
Cloning and sequencing of a gene for lactococcal endopeptidase, an
enzyme with similarity to mammalian enkephalinase
J. Bacteriol. 175, 2087-2096 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                           LACOPEP 2599 bp DNA BCT 14-JUL-1993 Lactococcus lactis peptide-binding protein and endopeptidase (oppA) and (pepO) genes, 3'end and complete cds.
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1 (bases 1 to 2580)
                                                                                                                                                                                                                                                                                                                                    endopeptidase; oppA gene; pepO gene; peptide-binding protein. Lactococcus lactis (individual_isolate P8-2-47, sub_species
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Hybrid insulin/IGF-I receptor mRNA.
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WO 9117252-A 26 14-NOV-1991;
Location/Qualifiers
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Location/Qualifiers
/organism="Lactococcus lactis"
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1. 375
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807 c 710 g
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/db_xref="taxon:32630"
733 c 699 g 551 t
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Local Similarity 100.0%;
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Rabbit prolactin receptor 2 mRNA, complete cds:
J04510
                                                                                                                                                Oryctolagus cuniculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Lagomorpha; Leporidae; Oryctolagus
1 (bases 1 to 2635)
                                                                                                                                                                                                                     prolactin receptor.
Rabbit (14-day pregnant) mammary gland,
PRLR-2[1,4].
                     Proc. Natl.
89184578
                                                                         Edery,M., Jollcoeur,C., Levi-Meyrueis,C., Dusanter-Fourt,I., Petridou,B., Boutin,J.-M., Lesueur,L., Kelly,P.A. and Djiane,J. Identification and sequence analysis of a second form of prolactin receptor by molecular cloning of complementary DNA from rabbit
                                                                                                                                                                                                                                                                                  J04510.1
   Draft entry and computer-readable sequence for [1] kindly provided
                                                         mammary gland
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/product="endopeptidase"
/product="endopeptidase"
/product="endopeptidase"
/product="endopeptidase"
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/db_xref="gi:293015"
/db_xref="gi:293015"
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/translation="syriqddefativnaewlenaeipadkprisafdelylkneknla
/translation="syriqddefativnaewlenaeipadkpriyrddefatirpdtryndehpkkell
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/translatirfdyenaeijaksalkfdallvesantsemakyaeijkhelifdsf
NNLTQLvfthgoafgerightylytedfatsferfesgeslineenwellkamultkiarg
syrvknldlkslikdlvftepdkvivgeaasgekholdltesyrsgviglevakyeelkfogag
rapykkhelifdgargefisknewlsgefatkkalikldaifpfgebostivfbaki
rtsgslyedalkfdgargefiskssekselshelbuktswhahmvnayysposniivfbakie
rqappyslegssgnyggigigylaheishafdbargekbullkaefesgwa
kokemialfdgveffbagpangklivseniaoggifaalfaakdekdulkaefesgwa
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/translation="phmttpdgandwditdgswslasepsqqdlfsasapynfghfnd
/translation="phmttpdgandwditdgswslasepsqqdlfsasapynfghfnd
Seitkdlwdisaksenfytrkaafvkyqedmnkkayvvptnfslsytpvnkrvvgmt
Ldygandtwseigvssaklatk"
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<1. .375
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/protein_id="AAA25203.1"
/db_xref="PID:9293014"
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Local Similarity 100.0%;
hes 9; Conservative
PD 19-NOV-1996
PE 28-APR-1995 JP 1995128881
PI HONSHIYO YUU, NAKANO TORU, SHIBAYAMA SHIRO, TADA HIDEAKI, PI
PUKUSHIMA DAIKICHI
PC C07K14/47,A61K38/00,A61K38/00,A61K38/00,A61K39/395,
PC A61K39/395,
PC C07H21/04,C07K16/18,C12N1/21,C12N15/09,C12P21/02, PC
C12P21/08/A61K48/00,
PC (C12N1/21,C12R1:19),(C12P21/02,C12R1:19);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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ONO PHAR
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PD 19-
PF 28-
PF HON
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818 bp upstream of BamHI site.
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1 (bases 1 to 2681)
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/db_xref="taxon:9986"
477. .548
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549. .2324
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DALQSSKTTEAAGEEKATKQREVESSHSKAEQDTGWLLPKEKPPFISFKPLDYVEIHK
VNKDGALSLLLKQKENGDQTGKAGTPETSKEYAKVSRVMDNNILVLVQDPGAQNVALF
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SPESSIQIPNDFTMKDITVWIFVAVLSTIICLIMVWAVALKGYSMVTCIFPPVPGPKI
KGFDTHLLEKGKSEELLSAFGCQDFPPTADCEDLLVEFLEVDDSEDQQLMPAHSKEHS
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VNATNQMGSSVSDPRYVDVTYIVEPDPPVNLTLEVKHPEDRKPYLWVKWLPPTLVDVR
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/db_xref="PID:g165670"
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d. No. 8.17e+03;
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Local Similarity 100.0%;
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S72373.1
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S72373
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This sequence comes from Fig. 1a.
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Relationship between Drosophila gap gene tailless
nuclear receptor Tlx
Nature 370 (6488), 375-379 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Archosauria; Aves; Neognathae; Gall
Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                        /organism="Gallus gallus"
/db_xref="taxon:9031"
328. .1485
                                                                                                    /note="tailless prote
protein Tll homolog.
                                                                                                                                                                            /note="tailless homolog; Drosophila terminal/gap gene
tailless homolog"
/translation="mskpagstsrildipckvcgdrssgkhygvyacdgcsgffkrsi
rrnrtyvcksgnqggcpvdkthrnqcracrlkkclevnmnkdavqhergprtstirkq
                         /product "nuclear receptor TLX"
/protein_id="AAB31467.1"
/db_xref="piD:9619338"
/db_xref="GI:619338"
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/db_xref="taxon:9606"
830 c 850 g 49
                                                                                                                                  /gene="Tlx"
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Pred. No. 8.17e+03;
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/cell_type='gliobastoma'
/cell_line='T98G'
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                                                                                                                  Tll homolog;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erratum:[[published erratum appears in Infect Immun 1998 May:66(5):2399]]
3 (bases 1 to 2704)
Bevins,C.L., Tarver,A.P., Diamond,G., Wines,M. and Hwang,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF016539 2704 bp DNA MAM 25-FEB-1
Bos taurus enteric beta-defensin (EBD) gene, complete cds.
AF016539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Somatic cell mapping of beta-defensin genes to cattle syntenic group U25 and fluorescence in situ localization to chromosome amanm. Genome 6 (8), 554-556 (1995)
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Gallagher, D.S. Jr., Ryan, A.M., Diamond, G., Bevins, C.L.
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AF016539.1
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (30-JUL-1997) Immunology, The Cleveland Clinic Foundation, 9500 Euclid Avenue, Cleveland, OH 44195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
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QPTPKYPHEVNGTPMYLYEVATESVCESAARLLFMSIKWAKSYPAFSTLSLQDQLMLL
EDAWRELFVLGIAQWAIFVDANTLLAVSGMNGDNTDSQKKINKIISEIQALQEVVARFR
QLRLDATEFACLKGIVTFYKAVPTHSGSELRSFRNAAAIAALQDEAQLTLNSYIHTRYP
TQPCRFGKLLLLLPALRSISPSTIEEVFFKKTIGNVPITRLLSDMYKSSDI"

8 681 c 638 g 658 t
                                                    /gene="EBD"
859. .885
                                859. .885
/gene="EBD"
                                                                                           /gene="EBD"
827. .831
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/gene="EBD"
                                                                                                                                                                                                                                                                                              /chromosome="27"
775. .780
                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
/db_xref="taxon:9913"
                   )oin(859.
                                                                                                                                                                /product="enteric beta-defensin"
312. .885
                                                                                                                                                                                                                                                                             /gene="EBD"
/gene="EBD"
                                                                                                                                               'gene-
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                 .943,2416. .2651)
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Pred. No. 8.17e+03;
0; Mismatches 0
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RESULT 153
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                                 g466381
U07694.1
                                                       Columba
U07694
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I13760.1
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domestic pigeon.
Columba livia
                                                                                                                                                                                                                                                     1 (bases 1 to 2713)

Queno,T., Ito,H., Kotani,H. and Nakajima,K.
NSP7524V restriction-modification genes
Patent: US 5441881-A 1 15-AUG-1995;
Location/Qualifiers
                                                                            CLU07694
                                                                                                                                                                 h 100.0%;
Similarity 100.0%;
9; Conservative
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                                                                livia prolactin
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/gene="EBD"
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/gene="EBD"
2632. .2637
/gene="EBD"
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1 649 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MRLHHLLTLLFLVLSAGSGFTQGTSNPLSCRLNRGICVPIRCP
GNLRQIGTCFTPSVKCCRWR"
                                                                                                                                                                                                                     organism-"unknown"
516 c 427 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="enteric beta-defensin"
/protein_id="AAC48804.1"
/db_xref="pID:92367667"
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8.17e+03;
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RESULT 154
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mat_peptide
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                                                                                                                            Gallus
M77638
Gallus gallus DNA.
Gallus gallus
Eukaryotae; mitoch
                                                                                        g211739
M77638.1 GI:211739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-MAR-1994) Xiaojuan Chen, Physiology & Biophysics, University of Cincinnati Medical College, 231 Bethsda Ave., Cincinnati, OH 45267, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prolactin receptor
Endocrinology 135 (1),
94283267
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1 (bases 1 to 2713)
Chen, X. and Horseman, N.D.
                                                                      elongation growth
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                                                        receptor
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NSHYYRYELAKKPERKEWETYSVGVQTQYKVNRLQAGVKYVQVGVCYDLDIGEWSENS
SERHIHIRNGESPPEKPTIKCRSPEKETTTCWMKPGSDGGHPTNYTLLYSKEGEERV
YECPDYKTAGPNSCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVDVTYLLYSKEGEERV
YECPDYKTAGPNSCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVDVTYIVQTDP
VNVTLELKKTYNRKPYLVLTWSPPPLADVRSGNLTLDVELALKYEDEAEKWETIFVGOO
THYKMFSLNPGKKYIVQIKCKPDHHGSWSEWSLEKYLQIPTDFRIKDMVWAIIVGVLS
SLICLYMSWTMVLKCYRMIAFTLPPVPGPKIKGIDTHLLETGKSEELLSALGCHGFPP
TSDCEELLIEYLEVEDSEDQQLMPSHDNGHPSKNAKMIAKETDSDSGRGSCDSPSLLS
EKCRESRAILSTLQTODIRDVGENNGRRHWETQCIASEGKILLFNRESTKSSIWPAAQ
LPDNQPPMFAYHSTVDVHKITLCTIDVNIAPVLVENEEDGHQPQVEITETTYHDMMEKHR
EVENLYSKTDGTTVQVKQNRPNDKSPFSKPKLMDYVEVHKVRQDEVAAVLLKHKENSG
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KIEKYTVPGTSKEXTNYSTVVDHNILVLMPDSRIQHIFVSQEPAMEMSQNLQQGGTEK
                                                                                                                                             gallus
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2672. .2713
554 c 575 g
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/translation="MKQKLRSVQIILLFALTAVGLTGQSYPGKPKIIRCRSLEKETF
/translation="MKQKLRSVQKITCFCFDYGMSGPNSCYFDKNHTNPWTTYNIT
SCWWKPGSDGGLPTNYTLFYSKDSEEKIYECPDYGMSGPNSCYFDKNHTNPWTTYNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="assembled from a clone of pigeon crop lambda
gtll cDNA library and a PCR product"
/tlssue_type="crop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NMSYCLTVPSECKRETSASEYMDPSSFIPAFK"
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/protein_id="AAA20646.
/db_xref="PID:g466382"
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   mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                            2723 bp DNA VRT EGF/TGF-receptor (c-erbB) gene,
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                                                                       receptor;
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Bos taurus (clone: Sal3.8
Bos taurus
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L42319.1
          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; I Bovidae; Bos.

1 (bases 1 to 2742)

Taylor,G.A., Thompson,M.J., Lai,W.S. and Blackshear,P.J. Phosphorylation of tristetraprolin, a potential zinc fing transcription factor, by mitogen stimulation in intact comitogen-activated protein kinase in vitro 95286626

J. Biol. Chem. 270 (22), 13341-13347 (1995)
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FilckInger.T.W., Maihle,N.J. and Kung,H.-J.
An alternatively processed mRNA from the avian c-erbB gene encodes a soluble, truncated form of the receptor that can block ligand-dependent transformation Mol. Cell. Biol. 12, 883-893 (1992)
                                                                                                                                                                                                                                                                                                                   BOVZPF36G
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(bases 1 to 2742)
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/gene="c-erbB"
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db_xref="taxon:9031"
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Mismatches 0;
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                                              A2749774
AB004650.1 GI:2749774
AB004650.1 GI:2749774
Alternative splicing; CENP-C; centoromere protein C.
alternative splicing; CENP-C; centoromere protein C.
Gallus gallus cDNA to mRNA, clone:CENP-C_1_2.
Gallus gallus
Eukaryos Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Eukaryos Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Eukaryos Metazoa; Chordata; Phasianinae; Gallus.
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Chicken mRNA for CENP-C,
AB004650
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Promoter
Direct Submission Submitted (10-JUN-1997) to the DDBJ/EMBL/GenBank databases. Tatsuo
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                                         Fukagawa, T.
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/gene="zpf-36"
/gene="zpf-36"
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KTELCRTFSESGRCRVGAKCOPAHGLGELRQASRHPKVKTELCHKFYLOGRCPYGSRC
HFIHNPSEDLAAPGHPHVLRQSISFSGLPSGRRTSPPPASLAGPSVSSWSFSPSSSPP
PPPGDLLLSPSAFSAAPGHLCRRDPTPACCPSCRRATPNSVWGPVGGLARSPSAHSLG
SDPDEYASSGTSLGGSDSPVFEAGVFGPPQPPAAPRRLPIFNRISVSE"
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162. .:
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/note="(vector lambda DASH II)"
/db_xref="taxon:9913"
/clone="Sal3.8"
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/protein_id="AAB05819.1"
/db_xref="pI::91100071"
/db_xref="GI:1100071"
/translation="MDLAAIYKSLLSLSPELPSDLGETESSTSWASSGPWSLSSSDSS
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gene="zpf-36"
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Jenkins,N.A., Gilbert,D.J.,
Lefkowitz,R.J.
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M73216.1 GI:162734
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                                                                                       Cloning expression, and chromosomal localization of beta-adrenergic receptor kinase 2: A new member of the receptor kinase family J. Biol. Chem. 266, 14939-14946 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOVBARK 2791 bp mRNA MAM 05-SEP-1991 COW beta-adrenergic receptor kinase 2 (beta-ARK2) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
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//protdin_start=1
//protdin_id="CENP-C"
//protdin_id="SA244110.1"
//db_xref="pID:d1025017"
//db_xref="pID:d1025017"
//db_xref="pID:d1025017"
//db_xref="pID:d249775"
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/db_xref="taxon:9031"
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                                                                                                                                                                                                                                       Targeting of endopeptidase 24.16 to different subcellular compartments by alternative promoter usage J. Biol. Chem. 272 (24), 15313-15322 (1997)
                                                                                                                                                                                                                                                                                                                                          Submitted (27-DEC-1996) to the DDBJ/EMBL/GenBank databases. Shigehisa Hirose, Tokyo Institute of Technology, Department o Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726, Fax:045-924-5824)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Ma
Artiodactyla; Suiformes; Suina; Suidae; Sus.
1. (bases 1 to 2810)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB000172.1 GI:1783126 endopeptidase 24.16 type M2; endopeptidase 24.16 Sus scrofa Adult Liver cDNA to mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                           (Sites)
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FPLVISERWQQEVAETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGRDCIVHGYML
KLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQSLLTMEQIVSVEETQIKDKKCILLRI
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/organism="Bos taurus"
/db_xref="taxon:9913"
49. .215
                  /note="corresponding to exon2,5-16 of this gene;
endopeptidase 24.16 type 2"
130. 2367
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QHKTKDKHEIDRWTLTMNVELPDVFSPELKSLLEGLLQRDVSKRLGCHGGSAQELKTH
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MKCLDKKRIKMKQGETLALNERIMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNG
GDLHYHLSQHGVFSEKEMRFYATEIILGLEHMHNRFVVYRDLKPANILLDEHGHVRIS
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CRSRQIYDTYIMKELLSCSHPFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGS
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49. .2115
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/protein_id="AAA30406.1"
/db_xref="pID:9162735"
/db_xref="GI:162735"
/translation="MADLEAVLADVSYLMAMEKSKATPAARASKKIVLPEPSIRSVMQ
                                                                                                                                                                                                 Location/Qualifiers
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/standard_name="endopeptidase 24.16"
                                                                                                                   /db_xref="taxon:9823"
/dev_stage="Adult"
                                                                                                                                                           organism="Sus scrofa"
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                                                                                              'tissue_type="Liver"
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d. No. 8.17e+03;
Mismatches 0;
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D88363.1 c
cm19; M1tf.
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D88363
                                                                                                                Gallus gallus (strain:White leghorn) 9-day-old embryo retinal pigmented epithlium cDNA to mRNA.
                            Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Ave
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                       Gallus gallus
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Similarity 100.0%;
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(bases 1 to 2863)
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AASTEADKRLSRFDIEMSMREDIFLRIVRLKETGDLĞKIK PEARAFLEKSVKMGKRNG
LHLPBOVQNEIKAMKKNESLCIDETRIKNILENDITELVFSKAELGALPDDFIDSLEKTIG
DNKYKITLKYPHYFPVMKKCCIPETRKMEMAFNTCKEENTIILQELLPLRAKVAKL
LGYSTHADFVLEMNTAKSTHHYTAFLDDLSQKLKPLGAREREFILNLKKKECEEKGFE
YDGKINAMDLHYYMTOTEELKYSVDQBILKEYFPIEVVTEGLLNIVQBLLGLSFEQVT
DAHVMNKSVTLYTKNDKATGEVLGQFYLDLYPEGKYNHAACFGLQPGCLLPDGSRM
SVAALVVNESQPRAGRESLLRHDEVRTYFHEFGHVMHQICAQTBARFSGTNVETDFV
EYPSQMLENNVUDTDSLRRLSKHYKDGSFITDDLLEKLVASLVUTGLLTLRQIVLSK
VQSLHTNTSLDAASEYAKYCTEILGVAATPGTNMPATFGHLAGGYDGQYGYLMSEV
VGSMDRYSCFKKEGIMNPEVGMKYRNLILKFGGSLDGMDMLQNFLKREPNQKAFLMSR
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angiotensin-binding protein) :MEP(microsomal
metalloendopeptidase)"
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LENWVWDTDSLRRLSKHYKDGSPITDDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLH
TNTSLDAASEYAKYCTEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMF
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AWDLHYYMTQTEELKYSVDQEILKEYFPIEVVTEGLLNIYQELLGLSFEQVTDAHVWN
KSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMSVAALV
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/db_xref="pid:d1019807"
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/db_xref="gi:1783128"
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/tryvddighldiefytyfenciaalavevkriverrwldfpodskevraastea
rkyvtddighldiefytyfenciaalavevkriverrekterryldfpodsidslektdbukykri
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/translation="MYYPEGHLARELGATFSSSAPLGGHPFPFVWDCLSCKQGDWSQA
RPKINAERRSGVGGSGILLRWTLGREAMSPLQAMSSYTVDGRNVLRWDLSPEQIKRRT
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/note="alternative product for this mRNA; oligopeptidase M
:neurolysin :sBAP(soluble angiotensin-binding protein)
:MEP(microsomal metalloendopeptidase)"
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                                                                                                                                                                                                       GI:3061279
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/db_xref="PID:g1783127"
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inserterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2873)

Geyer, P.K. and Corces, V.G.
separate regulatory elements are responsible for the complete pattern of tissue-specific and developmental transcription yellow locus in Drosophila melanogaster Genes Dev. 1 (9), 996-1004 (1987)
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Drosophila melanogaster
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                                                                    author numbering refers to yellow transcription start site at \pm 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
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135. .1541
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/db_xref="taxon:9031"
/dey_stage="9-day-old embryo"
/tissue_type="retinal pigmented epithlium"
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/db_xref="PID:d1026579"
/db_xref="PID:g3061280"
/db_xref="GI:3061280"
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Sequence 2 from Paten
A44216
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/db_xref-"FlyBase:FBgn0004034"
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/db_xref="FlyBase:FBgn0004034"
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/db_xref="taxon:32630"
533 c 639 g 786 t
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/db_xref="FlyBase:FBgn0004034"
1007. .2176
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/map="type 2 allele"
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gene="y"
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0; Mismatches 0
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"PRODUCTION OF ACTIVE HUMAN ALT";
Datent number JP 1996103278-A/3, 23-APR-1996.

OR ARTIFICIAL Sequences.

PN JP 1996103278-A/3

PD 23-APR-1996

PI NAKAMURA ATSUO, TANAKA TOSHIO, MATSUO TAKESI
PI FUNATSU MASAHIKO, ETO AKIRA
PC C12N15/09,C07H21/04,C07K14/47,C12N1/21,C12N1

PC G01N33/573,
PC (C12N1/21,C12R1:19),(C12N9/10,C12R1:19);
PC G12N3/573,
PC (C12N1/21,C12R1:19),(C12N9/10,C12R1:19);
PC Strandedness: Double;
PC topology: Circular:
FH Key

FT source
FT source
FT promoter
FT consoler 1.2927
FT consoler 267.326
FT consoler 267.326
FT CDS /product="beta-lactamase"
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Local Similarity 100.0%;
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07-OCT-1994 JP 1994268119
07-OCT-1994 JP 1994268119
NAKAMURA ATSUO, TANAKA TOSHIO, MATSUO TAKESHI, TANASE SUMIO, FUNATSU MASAHIKO, ETO AKIRA
C12N15/09,C07H21/04,C07K14/47,C12N1/21,C12N9/10,G01N33/53,
                                                                                                                                                                                                                                                                 g1022699
U33888.1
                                                                                                1 (bases 1 to 2939)
George, J.M., Seld,C.A., Lee,H. and Tomlinson,C.R.
Two distinct forms of USF do not appear to play a role in the inactivation of the LpS1 genes when the extracellular matrix disrupted in the Lytechinus sea urchin embryo Unpublished (1995)
2 (bases 1 to 2939)
                                                                                                                                                                                      green urchin.
Lytechinus variegatus
Lytechinus variegatus
Eukaryotes; Metazoa; Echinodermata;
Echinozoa; Echinoidea; Euechinoidea; Echinozoa; Temnopleuroid
Toxopneustidae; Lytechinus.
                                                                                                                                                                                                                                                                                          Lytechinus
U33888
                                                  Houston,
                                                               Submitted (14-AUG-1995)
                                                                         Direct Submission
                                                                                       George, J.M.
                                                                                                                                                                                                                                                                                                                   LVU33888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unidentified"
/db_xref="taxon:32644"
/BP; 725 A; 736 C; 718 G; 748 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                     25
                                                Houston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
/organism="Lytechinus variegatus"
/note="green urchin"
                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                      variegatus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Artificial sequences" 267. .326 /note="trp promoter derived from 1127. .1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTRF
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                                                  TX 77
                                                                                                                                                                                                                                                                                                     mRNA
S USF mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9; DB 11;
Pred. No. 8.17e+03
0; Mismatches
                                                  ) Jenny M.
7204-5513,
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                                                   George,
USA
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U21155.1
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2841 TTCTCAGAA 2849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 2948)
Wigle, J.T., Demchyshyn, L., Sattar, S., Pratt, M. and Tuana, B.S.
Molecular Cloning of a Novel Family of Sarcolemmal Associated
Coiled-Coil Proteins: Protein-Protein Interactions at the Cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus
Oryctolagus cuniculus
Eukaryotae; mitochondrial eukaryotes; Metazoa;
Eukaryotae; mitochondrial eukaryotes; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus complete cds.
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Similarity 100.0%;
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                   /translation="MDEQDLNESLAKVSLLKALLEEERKAYRNQVEESSKQIQVLQAQ IQRLHMDIENLREEKDNEITSTRDELLSARDEILLHQAAEKAASERDTDIASLQEEL KKVRAELERWRKAASEREKENTSLQSEFQLRCQCEDQXKEEATRLQGELEKLRKEWN VLETECHSLKKENVLLSSELQRQEKELHNSQKQSLELTSDLSILQMTRKELENQMGSL KEQHLRDSADLKILLSKAENQAKDVQKEYEKTQTVLSELKLKFEMTEQEKQSITDELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAA79690.1"
/db_xref="piD:9102700"
/db_xref="piD:9102700"
/db_xref="giD:9102700"
/translation="MTLYQTSYQYIYIFHTYTGTSTTYFFFGYTSGIPNIHDKDKDLD
EVANHLTADGDQVYTDPSGEGFFADMIQYQFRTDSNGQSQVTRVVQVGDTESNPQA
VYTTFPQGQQALTQVMEGSSNGESPTSERGGETRFTYFPAASAMGGDGGGTASGGEQ
GGIAAQPTGSSGGQFYYMMSPQDVLQGASQRTIAPRTHQFNTKYDSARTYDBERRAF
HNEVERRRRDKINNWIVKLSKIIPDCNIDHSKQGQSKGGILSKTCDYIQELRQSNTRM
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883. .1854
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567 c 601 g 846 t 16 others
QCKDNLKLLQEKGNNNKPWPWMPMLAALVAVTAIVLYVPGLARASP"
                                                                                                                                                                                                                                                                                                               /gene-"SLAP1"
189. .1157
                                                                                                                                                               /product="sarcolemmal associated
/protein_id="AAA65598.1"
/db_xref="PID:9790240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryctolagus
/db_xref="taxon:9986"
/clone="SLAP1"
                                                                                                                                           /db_xref="GI:790240"
                                                                                                                                                                                                                                    /evidence=experimental
                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                   /gene="SLAP1"
                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="heart"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
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BASE COUNT 965
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Gallus ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-JUN-1997) to the DDBJ/EMBL/GenBank databases. Tatsuc Fukagawa, University of Oxford, Department of Biochemistry; South Parks Road, Oxford Ox1 30U, UK (E-mail:tfukagaw@bloch.ox.ac.uk, Tel:44-1865-275225, Fax:44-1865-275259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alternative splicing; CENP-C; centoromere protein C. Gallus gallus CDNA to mRNA, clone:CENP-C_5_3. Gallus gallus Chordata; Vertebrata; Archosauria; Aves; Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
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1 (bases 1 to 2952)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukagawa, T. and Brown, W.R.
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/function="anchors protein to membrane"
/product="hydrophobic carboxyl tail"
2923...2928
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/product="leucine zipper-like motif"
1080. .1130
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/product="leucine zipper-like motif"
7,77. . 842
                                                                                                                                                                                                                                                                                                                    /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="CENP-C_5_3"
                                                                                                                                                                                                                                  /product="CENP-C"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       conditional mutation of the vertebrate CENP-C gene Genet. 6 (13), 2301-2308 (1997)
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                                                                                                                                                                                                                                                                                         note="alternative splicing: see also AB004650"
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alpha subunit; flpF gene; formate dehydrogenase.
Methanobacterium thermoautotrophicum.
Methanobacterium thermoautotrophicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (15-JUN-1995) A. Hochheimer, Max-Planck-Inst. fuer
Terrestrische, Mikrobiologie, Karl-von-Frisch-Str., 35043 Marburg,
FRG
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THANS I AT LON-"MIGTYKE ALDGREVEAARGMTVLEAALANGIYI PNLCFREGIEP

FIGGCRLCLVENNEGRLVTACETPAEDOSSEFI SESERINRI RRTTLSLII ADHSRDCLA

FIGGCRLCLVENNEGRLVTACETPAEDOSSEFI SESERINRI RRTTLSLII ADHSRDCLA

CPASGDCRLQELSSYLNVSDGDLERLRPELSGIDVDESNPFFLRNHDKCIICGICVRV

CRGLGAEAVDFAYRGHDTRIATFMDRDILDSSCVSCGECVEACPVGALLPRTERPSTE

VRTVCPYCGAGCEIYLGVRGNRVVSSRGVPDSPVNOGRLCVKGRRALKFVNSPERLKK

PLIKVDGEFVEVEMDEAISVVAERLSEXTGEEEFAAVASAKCTINEENYLLOKFTRAVMG

FILKVDGEFVEVEMDEAISVVAERLSEXTGEEFAAVASAKCTINFTETHPVTSYR

SGNIDHCARLCHAPSLTGLNKSLGSGAMTUSISELGAACCILAVGTUPTETHPVTSYR

VIRALRSRARLVVVDPRKTRLSELADIHLQNRPGSDIPLLMAMCRFILEEGLHDSEFI

DSRTEKFEDERDAVMALDLDEVERITGVNVKDIKRAALMYSASSPASII YSMGITQHV

NGTGNVLALSNLALLTGNIGIKSAGINLFRGQNNVQGACDMGALDDLDGVGGIGEAA

GKFSEKWGSPIPPAGLTLPEMTDAARDGKIRCMYIMGENFLLSEDDIERTREALEGLE

FLVYQDICLTETAELADVYLPAASFAEKDGTTNTERRYOLLRKALDAAFGDALPDWGI

FILVYQDICLTETAELADVYLPAASFAEKDGTTNTERRYOLLRKALDAAFGDALPDWGI

FLVYQDICLTETAELADVYLPAASFAEKDGTTNTERRYOLLRKALDAAFGDALPDWGI
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VVIRGQIITTLHKTSYYLTSGDYFYVPAGNGYNIRNLLNEESVLHFTQLKNDRAFVGA
ELCSVTNENWSLEGKS"
2930. .2552
a 588 c 683 g 705 t
                                                                                                                                                                                                                                                                                                      /product="putative alpha subunit of formate dehydrogenease" protein_id="CAA61208.1" /db_xref="PID:9871456" /db_xref="GI:871456" /db_xref="SPTREMBL:050743"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="fl
134. .279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Methanobacterium thermoautotrophicum'/strain="Marburg/DSM 2133"
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134. .2797
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d. No. 8.17e+03;
Mismatches 0
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150971
92472674
150971.1 GI:2472674
                                                                                                                                                   Submitted (18-OCT-1996) A.C. Mintzas, University of Patras, Department of Biology, Patras, 26500, GREECE 2 (bases 1 to 3005)
                                                                                                                                                                                                                           Mediterranean fruit fly.

Ceratitis capitata

Ceratitis capitata

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecretrygota; Diptera; Brachycera; Muscomorpha; Tephritoidea;

Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                                                   C.capitata gene encoding Y08955
                                                                                                                                                                                                                                                                                               HSP70 protein.
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Y08955.1 GI:1894775
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Hammock, B.D., Hanzlik, T.N., Harshman, L.G., Bonning, B.C.
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                                                                                                                           Unpublished
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                                                                                                                                          Mintzas, A.C.
                                                                                                                                                                                         Direct Submission
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; US 5643776-A 1 01-JUL-1997;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unknown" 625 c 636 g
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                                                                                                               Location/Qualifiers
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g for HSP70 protein.
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U21156
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Submitted (15-FEB-1995) Jeffrey T.
of Ottawa, 451 Smyth Road, Ottawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 3020)
Wigle, J.T., Demchyshyn, L., Sattar, S., Pratt, M. and Tuana, B.S.
Molecular cloning of a novel family of sarcolemmal associated
coiled-coil proteins: protein-protein interactions at the cell
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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TKACDDTIKWLDATRLADKEEYEDKMNTLTKLCTPIMTKLHSGGGAGQGASCGQQAGG
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/transi_table=11
/product="cytotoxic protein"
/protein_id="AAA,99268.1"
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1152 1202
/note="encodes a hydrophobic carboxyl tail"
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1 (bases 1 to 3104)

Hoeltke, H.J., Seibl, R.,
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2 (Wang, H.-F., Kim, J., Huang, Y.K. and Lin, M. Direct Submission
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1 (bases 1 to 3030)
Kung.H.-F., Kim.J., Huang,Y.K. and Lin.M.C.
Molecular cloning of two different forms of
                           Method for the detection of nucleic Patent: EP 0324474-A 4 19-JUL-1989;
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Anura; Mesobatrachia; Pipoidea; Pipidae;
BOEHRINGER MANNHEIM GMBH
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/protein_id="AAD03594.1"
/db_xref="pID:g4118837"
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/db_xref="taxon:8355"
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Center, Frederick, MD 21702-12
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X58386.1 GI:162
dissociable hydrophilic catalytic complex (V1); H+-ATPase subunit; vacuolar H(+)-ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (12-AUG-1991) G.E. Dean, Univ of Cincinnati Submitted, Dept of Mol Genetics-Biochem and Micro, 231
Avenue, Cincinnati Ohio 45267-0524, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BTBVATPA 3106 bp mRNA 1
B.taurus mRNA for bovine vacuolar ATPase subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan,Y.X., Xu,J., Strasser,J.E., Howell,M. and Dean,G. Structure and expression of subunit A from the bovine cell vacuolar ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; 1 (bases 1 to 3106)
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                                                                       /db_xref="taxon:32630"
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                                                   TLEVAKLIKDDFLQQNGYTPYDRFCPFYKTVGMLSNMIAFYDMARRAVETTAQSDNKI
TWSIIREHMGEILYKLSSMKFKDPVKDGEAKIKADYAQLLEDMQNAFRSLED"
                                                                                                                                                                                                                        /product="H(+)-transporting ATPase"
/protein_id="CAA41276.1"
/db_xref="PID:g163"
                                                                                                                                                                                                                                                                                                                                          /tissue_type="adrenal medulla"
/cell_type="chromaffin cell"
/clone_lib="Lambda ZAP chromaffin cell cDNA library"
/clone="Bluescript SK(-) plasmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                            /db_xre
                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                            /note="H(+)-ATPase subunit A"
                                                                                                                                                                                                                                                                                         /EC_number="3.
                                                                                                                                                                                                                                                                                                                                                                                                organism="Bos taurus"
/db_xref="taxon:9913"
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Pred. No. 8.17e+03;
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AJ001614.1
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AJ001614
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             'db_xref="SPTREMBL:Q00626"
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCRIFE----
Direct Submission
Submitted (15-SEP-1997) Schlieper D.,
Submitted (15-SEP-1997) Schlieper D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ001614.1 GI:2769261
ampicillin resistance;
activator protein; crp
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Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A positive selection vector for cloning of long reaction fragments based on a lethal mutant of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Cologne, Weyertal 121, Cologne, 50931, GERMANY 2 (bases 1 to 3128)
Schlieper, D., von Wilcken-Bergmann, B., Schmidt, M., Sobek, H. and
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Escherichia.
'hases 1 to 3128)
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                                                                                                                                                                                                                                              /transl_table=11
/evidence=experimental
/product="cyclic AMP receptor protein"
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/protein_d="CA004867.1"
/db_xref="PID:e1231197"
/db_xref="PID:e2769262"
/db_xref="SPTREMBL:052983"
/db_xref="SPTREMBL:052983"
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KGSYAVLIKDEEGKEMILSYLNGGDFIGELGLEEEGGEESAWVEAKTACEVAEISYKK
FROLIQVNEDILMRLSAQMARRLOVTSEKVGNLAFLDVSGRIAQTLLNLAKOPDAMTH
PDGMQIKITROEIGQIVGCSRQTVGRILKMLEDQNLISAHGKTIVVYGTR"
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                                                                                                                                                                            /direction=BOTH complement(2072./gene="bla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /plasmid="pCAPs"
/db_xref="taxon:562"
complement(315. .947)
                                                                                                                                      complement(2072.
/gene="bla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(315. .947)
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/protein_id="CAA04868.1"
/db_xref="PID:e1231198"
/db_xref="PID:g2769263"
/db_xref="GI:2769263"
                                                                                                                codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="crp'
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gene; cyclic amp receptor
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G.gallus mRNA for Chira
X99375
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1 (bases 1 to 3144)

Roberts,C., Daw,S., Halford,S., Whiting,J.A. and Scambler,P. Cloning and developmental expression analysis of chick hira (Chira) and developmental expression analysis of chick hira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-1996) P.J. Scambler, Institute of Child Health, 30 Guilford St, Room 214, London, WClN 1EH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus
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Mamm. Genome In press
2 (bases 1 to 3144)
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Similarity 100.0%;
                      900
              SWILNGLGILVCSMOGSVAFLNSSQDELGDPLTEEENSPFYHSTYGKSLPIMTDAQLS
TIT IENPEMSQAIEQROQOQAEOKNASIREMGTTTSVAGIVNGESLEDILKNLFKO
VETRTADGRRRITPLCIAQLDTGDFSTAFFNSIPLSGTLAGSIMSSHSNQQLMSLDSN
AANSENTSKESAEPVAAASVKETDDAANKDSVNATSVSTAPPASSSSVLTTPSKIEPM
KAFDSRFTERSKATSGSAVVTNTNQTVVDRLKDQNFIKENKPKDILLESSDSEEKIPV
AKPLSAPKRKLELEGETVEKKKKGRPKDSRLVPVTLTVQSPAALVSEKDAAWLSAPA
LALKLPTPIPOKSFTLQVSSDPSMYLEVENEMTTVGGSKLSRLKGNREGKEMETVLTS
RILTAAGSCEKYCVACEKRMQSYVSDCGRRLLPPILINTPISTIHGTGSYIMTLTTAA
TLSVMDVHKQTVIVREESLQTILSGSETTVSQILLTQHGIAVLALSEGKAYCSNPSLS
TWNLVSDKQDSLAQCADFRSSLPSQEAMLCSGPLTVIQGETSNSGRQAARLFSMPHLV
QQETTLAYLENQIAACHOSHEYRHWLLIYARYLVNEGFEYRLRELCKDLLGPVHY
STGSQNESTVMCIKRELKELLFVIGQNURFGREFTEYCEQLDIL"

00 a 711 c 767 g 764 t 2 others
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/db_xref="FID: g1890559"
/db_xref="GI:1890569"
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VKFPELLATLKGHSGLVKGLTWDFVGKTLASQADDRSLKVWRTWDGQLETSITKFFDE
CGGTTHVLRLSGSPDGHYLVSAHAMNSGFTAGIIERDGKXINNDFVGHRANTVVKE
CGGTTHVLRLSGSPDGHYLVSAHAMNSGFTAGIIERDKYNNDFVGHRANTVKG
CGGTTHVLRSGSPDGHYLVSAHAMNSGFTAGIIERDKYNNFGHRANTVKF
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1 773 c
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/db_xref="taxon:9031"
/dev_stage="12"
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2, (bases 1 to 3150)
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Eukaryota; Metazoa; Nematoda; Secernentea;
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Liebau, E., Wildenburg, G., Brophy, P.M., Walter, R.D. and
Henkle-Duhrsen, K.
Biochemical analysis, gene structure and localization
glutathione S-transferase from Onchocerca volvulus
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Direct Submission
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1 (bases 1 to 3150)
Liabau, E., Wildenburg, G., Brophy, P.M., Walter, R.D.
Henkle-Duhrsen, K.
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RMIYMAYETEKDPYIKSILPGELAKFEKLLATRGNGRNLILGDKISYADYALFEELDV
                                                                         /number=2
1302. .138
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/db_xref="GI:975211"
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724. .757
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|160. .1301
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Streptococcus pneumoniae.
Eubacteria; Firmicutes; Low G+C gram-positive bacteria;
Streptococcaceae; Streptococcus.
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Cheng, O., Campbell, E.A., Naughton, A.M., Johnson, S. and Masure, H.R.
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                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-OCT-1996) Laboratory of Molecular infectious diseases, The Rockefeller University, 1275 York Ave., New
                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                           /gene=
811. .
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DKASESENQKILEIEGQRILSKIADRDFVIVLAIEGKTFFSEEFSKQLEETSIKGFST
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2535. .25
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                                                                                                                                                                                                                                                                                      /note="uncapsulated"
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                                                                                                                                                                                                                                                                                                                      /organism="Streptococcus
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function="competence stimulating peptide precursor"
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IVFDFPLYILYLDGLGIERFLFPLGLYSYFRWMKQYERDRGLFLSLLLSLLYESTHNF
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/product="ComC"
957. .2282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLEIVFYEDHRCPISRLKIRKLKDILEKKSQK"
425 c 603 g 1049 t
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2279. .3031
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VFFALLLHIVSEVSDMYSTIKELNESGSILSSIVESJKITEFAMNSHKVQMEKEIA
LKOKKEDRHIYRITQUEIVELKELGEFEHDYAGMLYSDLLTEFAMNSHKOLDIRIYMEV
LVKANHKLRSDKYTYFDLNNIEDSALRSLVAQSIVYARNNGVEFTLEVKDTITKLPIE
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957. .2282
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/gene="comE"
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histidine kinase homolog"
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/product="ComE"
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/db_xref="PID:g1666906"
/db_xref="GI:1666906"
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/product="ComC"
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d. No. 8.17e+03;
Mismatches 0;
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Matches 9; Conservative
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Y08865.1
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Xenopus laevis
Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia;
Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia;
Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

1 (bases 1 to 3299)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (17-OCT-1996) C.D. Gove, Kings College, University Of London, The Randall Institute, 26-29 Drury Lane, London, WC2B 5RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erratum:[[published erratum appears in EMBO J 1997 Apr 1;16(7):1806-7]]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATA-6 gene; GATA-6 protein.
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X.laevis mRNA for GATA-6
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                                                                                                                                                                                                                                                  /product="GATA-6 protein"
/protein_id="CAA70088.1"
/db_xref="pID:e275165"
/db_xref="pID:91621281"
/db_xref="GI:1621281"
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874 c 1030 g
                                                                                      VVTSSLMSAQQTGSASPDSNILKYTGQDGLYSAVSLSSASEVAASVRQDSWCALALA"
813 c 661 g 883 t
                                                                                                                                                                               /db_xref="SWISS-PROT:P70005"
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/SISYLOGTGASQGTHSVASHWSQATSESSSYSSSSPHPSSRYHYSPSPPMANGSTRDT
GYSSSLAVSGRDQYAPLARPLNGSYGSPYTPYMTPQLTSAWPAGPFDNTMLHSLQSRG
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LIKPQKRVPSSRRIGLACANCHTTTTLWRRNTEGEPVCNACGLYMKLHGVPRPLAMK
KEGIQTRKRKPKNLNKSKSSSNGNSSHHITMTPTSTTSSTNSDDCIKNGSPSQNTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xenopus laevis"
/db_xref="taxon:8355"
/dev_stage="adult"
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1. .3299
                                                                                                                                                                                                                                                                                                                                                           'gene="gata-6"
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 Score
Pred.
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Pred. No. 8.17e
0; Mismatches
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d. No. 8.17e+03;
Mismatches 0;
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8.17e+03;
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VIBAGAB 3323 bp DNA BCT 05
Vibrio sp. agaB gene for beta-agarase, complete cds.
D21202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Organization and expression of three genes from the silkmoth early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Lepidoptera; Bombycoidea;
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1 (bases 1 to 3317)
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                                                                                                                                                                                                                                      991 a
                                                                                                                                                                                                                  /product="chorion protein"
991 a 645 c 657 g 1024 t
bp upstream of KpnI site.
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eggshell protein
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join(757...8
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                                                                                                                                                                                                                                                                   2220. .2681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="chorion protein"
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                                                                                                                                                        Score 9; DB 21; I
Pred. No. 8.17e+03;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yasushi Sugano
Sewater Science Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence analysis of the agaB gene encoding a new Vibrio sp. strain JT0107 Biochim. Biophys. Acta 1218 (1), 105-108 (1994)
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Sugano,Y., Matsumoto,T. and Noma,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-OCT-1993) to the DDBJ/EMBL/GenBank databases. Yasus Sugano, Japan Tabacco Inc., Seawater Science Research Laboratory; 4-13-20 Sakawa, Odawara, Kanagawa 256, Japan (Tel:0465-47-3161,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugano, Y
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Vibrio sp.
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                                                                                                           /translation="MVEVMKFTKNKIAALLSLTILLGVYGCGSTPSSSDAEGAVEDVGG
TIPDDE SAAFFKKVKKDHRKAEVVSDOGVTSGSSALKVNEDSVSEANKFKKWENNEVH
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PVEMLFNGTKRKLDGYMGGEKINLRNIYEFQIFVGPMDAQTVILDNENLYDATGDFI
EASGQEVKVSGPIPTVASITSFDEGQPTFVAFDRSAANTTELKTDMGGLLAVKLAAT
NAYPNIITKAPQPWDMSEYGDFSLAFDLESKADEPLQLFVRVDDAENEMGGTANGVV
DSMSSYVTLAFGDDGTTYLPLGQTGSQTVSGMRAEPPKKSYNAQAISYGMGEKSLDTS
NIVSFGLYKLQNFTKDAEFNIKGYRLIPNIDADATRYEGLIDQVGQFTGSEWPKKTTED
EELETMGKLAKMSLKSTSQMPGRSIYGGMADGFKLKGTGFFRTEKVDGKMSLVDPQGN
LFFATGVUNIRNDDTYVITGHDFADKDKRSGKEVASEVERSMFTMLJEDDDDYLAEBYD
YANNYHSGALKKGEVESFYGANLQRKVGGFTSBAEKVWRDTIDDBVDKGFTTLGWA
DPMFYDNKKVAYVANGWIFGDHARISTGNDYMGFINDSTYNSAAFTEHLKEKYWA
LEDLNTSWGKVASNAEFEKSEDHRSRLSKNMKKDYAEMLASAKYFSTYRAELKKY
IEDLNTSWGKVASNAEFEKSEDHRSRLSKNMKKDYAEMLASAKYFSTYRAELKKY
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RAWDGENYNVGFVSITDTPYVPLVEAAKKFNQDVYMLRYKK"
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259. 3126
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I44522.1
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guanylyl cyclase C.
Xenopus laevis adult intestine cDNA to mRNA, clone:xgcc2.1.
Xenopus laevis
                                                                                                                   Hokkaido University
Biological Sciences
Sapporo, Hokkaido 060
                                                                                                                                                                                                                            Submitted (24-MAR-1995) to the DDBJ/EMBL/GenBank databases. Ron T MacFARLAND, Hokkaido University, Biological Sciences; Sapporo, Hokkaido 060, Japan (E-mail:norto.suzuki@sl.hines.hokudai.ac.jp, Tel:011-706-4908, Fax:011-746-1512)
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus. 1 (bases 1 to 3493)
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Bennett,B.D., Goeddel,D. and Matthews,W.
Protein tyrosine kinase agonist antibodies
Patent: US 5635177-A 34 03-JUN-1997;
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Direct Submission
Submitted (07-JUL-1997) Marine Biology, Institute for Marine Submitted (07-JUL-1997) Marine Biosciences, 1411 Oxford Street, Halifax, NS B0J 1G0, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              Pleuronectes americanus
AF012465
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Douglas,S.E., Gallant,J.W. and Bullerwell,C.E.
Molecular Investigation of Aminopeptidase N Expression in the
Winter Flounder, Pleuronectes americanus
J. Appl. Ichthyol. (1998) In press
2 (bases 1 to 3517)
Douglas,S.E. and Gallant,J.W.
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Pleuronectes americanus
Pleuronectes americanus
Pleuronectes, Metazoa; Chordata; Vertebrata; Actinopterygii;
Eukaryotae; Metazoa; Chordata; Vertebrata; Actinopterygii; Percomorpha
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha
Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pleuronectes.
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                                         /organism="Pleuronectes americanus"
/db_xref="taxon:8263"
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Rosidae; Fabales; Fabaceae; Papillonoideae; Glycine.

1 (bases 1 to 3528)

Shibata, D., Kato, T. and Ota, H.

Shibata, D., Kato, T. and Ota, H.

DINA CODING NEW DNA-CONNECTED PROTEIN
Patent: JP 197224672-A 1 02-SEP-1997;
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK

OS Glycine max (soybean)
PN JP 1997224672-A/1
PD 02-SEP-1997

PP 21-FEB-1996 JP 1996033973
PF 21-FEB-1996 JP 1996033973
PF 21-FEB-1996 JP 1996033973
PF C12N15/09,A01H5/00,C07H21/04,C07K14/415//C12N5/10,C12Q1/68; CC
topology: Linear;
CC typothetical: No;
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E13668.1 GI:3252445
JP 1997224672-A/1.
Glycine max.
Glycine max.
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TTGLX1FTGSSTVEFKCTEDTDLILIBNKLNYTELDNGOWARLSAVNSGVKAPALXT
SRLQPVTQXLVLQLDGKLLKDQWYHLFTDFTGELADDLGGFYRSVYMENGLKXVVATT
QMQPTDARKAPPGFDEPAMKATTNITLHDPETVALSNCAQRESKRVTIDGKNLKQYD
FGQTEKMSTYLLAF1VSEFTSINNTVLNVLIRIFARKPAIDAGGGAYALSKTGPILKF
FEGYTRNSYPLPKSDQIALPDFNAGAMENWGLITYRETALLYDBAVSSNSNKERIATI
IAHELAHMWFGNLVLLRWWNDLMUNGGFASYVEYLGADVAEPDWNIKDLYVLNDVHRV
FAVDALASSHPLSAKEDDIQRPEQISELFDAISYSKGASVLRMLSDFLTEDIFVMGLR
TYLKEFAFGNAVTDLMNHLQMAVNATGTKLFGSVQDIMTWVLQMGFVVTINTTSG
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KTLYTUMTKVPTGHMDQYNQVNAISQAKTGHEECHTLVKGWFKKMDDTKINFTULDRIBNL
RTTVKONAIAAGGAKENDFAWSSFQNATIASEAEKLRSALACTTQPWLLQRYLEYTILD
RDKIRKQDATSTIVLANNVYGQSLAMDFVRDWSYIFNSALACTTQPWLLQRYLEYTILD
PDKIRKQDATSTIVLANNVYGQSLAMDFVRDWSYIFNSALACTTQPWLLQRYLEYTILD
PDKIRKQDATSTIVLANNVYGQSLAMDFVRDWSYIFNSALACTTQPWLLQRYLEYTILD
PDKIRKQDATSTIVLANNVYGQSLAMDFVRDWSYIFNSALACTTQPWLLGRYLEYTILD
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PDKIRKQDATSTIVLANNVYGQSLAMDFVRDWSYIFNSALACTTQPWLLGRYLEYTILD
PDKIRKQDATSTIVLANNVYGQSLAMDFVRDWSYIFNSALACTTQPWLLGRYLANNVYGGSLAMDFVRDWSYIFNSALACTTQPWLLGRYLANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATANNYGGNATAN
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/protein_id="AAG32754.1"
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/db_xref="piD:93452126"
/db_xref="GI:3452126"
/translation="MGKGFYISKAVGVVGVILGAGALATIIALSVVYSQEKAKNNNNE
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/EC_number="3,4.11.2"
/note="microsomal aminopeptidase; membrane alanyl
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Pred. No. 8.17e+03;
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/organism='Glycine max'
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RESULT 187
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I08049.1
                                                                                         Gallus gallus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 3643)
                                                       Yu,H.Y., Nettikadan,S., Fambrough,D.M. Negative transcriptional regulation of alpha 1-subunit gene
                                                                                                                                                     ATPase; Na+,K+-ATPase alpha subunit; Na, chicken.
                                                                                                                                                                                                   Gallus gallus
L43603
                                                                                                                                                                                                                          CHKNAKATPP
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Sequence 5 from Patent EP 0265293.
I08049
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1 (bases 1 to 3552)
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                                             Biochim. Biophys. Acta 1309 (3),
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'R 3384..3528.
Location/Qualifiers
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/organism="Gällus gallus"
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879 c 894 g
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/db_xref="taxon:3847"
716 c 865 g 10
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d. No. 8.17e+03;
Mismatches 0;
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H.giganteus hgiDIR & hgiDIM genes and ORF(metB)
enzyme HgiDIR and methyltransferase HgiDIM.
X55140
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I66488.1
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166488
              Dusterhoft, A., Erdmann, D. and Kroger, M. Stepwise cloning and molecular characterization of the HgiDI restriction-modification system from Herpetosiphon giganteus Nucleic Acids Res. 19 (5), 1049-1056 (1991) 91212183
                                                                                                                                                                                      Herpetosiphon aurantiacus
Herpetosiphon aurantiacus
Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 3656)
Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 8 23-SEP-1997;
Location/Qualifiers
                                                                                                        Submitted (27-NOV-1990)
Molekularbiologie, JLU
 See also X55137-X55143
                                                                                                                                     Direct Submission
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hgiDIM gene; hgiDIR gene; methyltransferase;
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Similarity 100.0%;
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772 c 869 g
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/sub_species="domesticus"
/db_xref="taxon:9031"
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HRHGSIADLANVLQQRLAKQSILVRDYFGLDTDYYYRHPRTYERRAIFSVNEPSPT
IRGVNRPIPATYRMHPKDAGDVYSLARPLTTKERSLIQTFPLDFKFVGTKSEQEQMIGN
AVPVNLAFFLATSLQAYLNQPRMQQLSLLPSFF"
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KTQGKLSILHENCLDLFVWSNFALAKVFLDASIKPSEKSITRPERTTVWLIKMLYDFA
QNGKIDYKRTLDRITFNLKNDKAFAASGMVTRKYMNSPELQNPRIKRHSIKHIIINGG
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sqnikpiyirlekrniehnyfavdqvfqinpleaqaffafehsyhpyteliigktpai
dvvisnlqnsqiinafeikltalipdnttanlpdnlqgceivirpdtivylalsiakvf
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/db_xref="PID:g581261"
/db_xref="GI:581261"
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/strain="Hpa2"
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Elsenberg, M.T., Kirkpatrick, R. and Rawls, J.
Structure of the rudimentary-like gene and UMP synthase in
Drosophila melanogaster
Gene 124, 263-267 (1993)
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Elsenberg, M.T., Gathy, K., Vincent, T. and Rawls, J. Molecular cloning of the UMP synthase gene rudime Drosophila melanogaster Mol. Gen. Genet. 222, 1-8 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscom Ephydroidea; Drosophilidae; Drosophila.
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Lonberg, N. and Kay, R.M.
Transgenic non-human animals for producing heterologous
Patent: US 5789650-A 120 04 AUG-1998;
Location/Qualifiers
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995 c 899 g
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615. .865
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1. .3710
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join(728. .865,926. .1442,2100.
/note="rudimentary-like"
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/strain="Canton S"
/note="Bienzyme protein containing catalytic domains for..
                                                                                  /db_xref="FlyBase:FBgn0003257"
join(728. .865,926. .1442,2100.
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/citation=[1]
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/tissue_lib="Maniatis Charon 4A"
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/db_xref="taxon:7227"
                               'EC_number="2.4.2.10"
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Query Match 100.0%;
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9468816
X78546.1 GI:468816
CAD gene; cadherin.
African clawed frog.
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X.laevis XB-cad mRNA
X78546
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3365. .3367
/gene="r-1"
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GIYKISSWADLYTAHTLPGRSILQGLKAGLGEGGAGKERGYFLLAEMSASGNLIDAKY
KENSNKIATEGADVDFYAGYYCQSSDAFAFPGLLQLTPGYKIDEGYDQLGQQYQSPEH
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YSLGLPQQTYSDLLVEHIKDKQLSAKHYGGVPYTALPRATIVSYQQGTPHLYRREDAK
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VANIAKHGVRHHSLFTLSFLLNTLHEAGRIEKSTYEAVAKYIAAVQINSDGTFVGGDK
YTFPAANDLQRTKLTYESRANLAKSAVAKRLFNLIASKQTNLCLAADLTHADEILDVA
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/citation=[1]
/evidence=experimental
875 c 914 g
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/protein_id="AAA29012.1
/db_xref="PID:9158794"
/db_xref="GI:158794"
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Muller, H.A., Kuhl, M., Finnemann, S., Schneider, S., van der Poel, S.Z., Hausen, P. and Wedlich, D.
Xenopus cadherins: the maternal pool comprises distinguishable members of the family
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Submitted (29-MAR-1994) M. Kuehl, University of Ulm, Department of Biochemistry, Albert-Enistein-allee 11, Oberer Eselsberg, 89081
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Expression of XBcad, a novel cadherin, during oogenesis and early
development of Xenopus
development of Xenopus
Mech. Dev. 35 (1), 33-42 (1991)
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Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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1772 c 873 g 1050 t 2 others
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LILSLLLLLFLKRKKVVKEPLLLPEDDTRDNIFYYGEEGGGEEDQDYDLSQLHRGLDA
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VFVPVVSRVDVSEDLTRGEKIVSLVAQDPDKQQIQKLSYFIGNDPARWLTINKDNGIV
TGNGNLDRESEYVKNNTYTVIMLVTDDGVPVGTGTGTLILHVLDINDNGPVPSPRVFT
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EPIPNLFTINRETGVISLIGTGLDREKFPEYTLTVQAADLDGAGLTAEGKAVIEITDA
NDNAPIFDPKTYTALVPENEVGFEVQRLSVTDLDMPGTAAWQAVYKIRVNEGGFFNIT
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LPVLTFPEKHTGLKRKKRDWVIPPIKVSENERGPFPKRLVQIKSNKEKLSKVFYSITG
QGADTPPEGIFRIEKETGWMQVTRPLDREEYEKVVLLSHAVSENCASVEEPMEITVTV
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/clone_lib="lambda zaj
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/db_xref="taxon:8355"
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S KHAN, M.A., HOTMBECHE, C.E., Chatfield, S.N. and Dougan, G.

S KHAN, M.A., HOTMBECHE, C.E., Chatfield, S.N. and Dougan, G.

S KHAN, M.A., HOTMBECHE, C.E., Chatfield, S.N. and Dougan, G.

S KHAN, M.A., HOTMBECHE, C.E., Chatfield, S.N. and Dougan, G.

ATTENUATED BACTERIA

Patent: WO 9504151-A 6 09-FEB-1995;

Patent: WO 9504151-A 6 09-FEB-1995;

MEDEVA HOLDINGS B V (NL)

Other publication PL 313979 960805

Other publication GB 2295394 960529

Other publication GB 2395394 960529

Other publication AU 2168459 950209

Other publication NO 950348 950328

Other publication AU 7235794 950328

Other publication AU 4713393 940303.
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  A37075 3769 bp DNA circular Sequence 18 from Patent WO9403615.
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Khan, M.A., Hormaeche, C.E., Villarreal-Ramos, B., Chatfield, S.N. and
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/db_xref="taxon:32644"
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Schistosoma mansoni.
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Etharyota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 3775)
Lantuer,F., Ziv,E., Ram,D. and Schechter,I.
Different forms of the mRNA encoding the heat-shock transcription factor are expressed during the life cycle of the parasitic helminth Schistosoma mansoni
T. Biochem. 253 (2), 390-398 (1998)
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                                                                                                                                                                                                                                                                                    2 (bases 1 to 3775)
Lantner, F., Ziv, E., Ram, D. and Schechter, I.
Direct Submission
Submitted (20-JAN-1998) The Weizmann Institute of Science, Rehovot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMHSF3 3775 bp DNA INV 21-MAY-1998 Schistosoma mansoni heat shock transcription factor, exons 6-10 and alternatively spliced products, complete cds.
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Khan, M.A., Hormaeche, C.E., Villarreal-Ramos, B., Chatfield, S.N. and
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/dev_stage="adult worm"
join(AF043419.1:915. 1073, AF043419.1:1107. .1215, AF043419.1:1249. .1667, AF043419.1:1702. .1846, AF043429.1:1249. .1667, AF043419.1:1747,1787. .263. .2812,3232. .3580)
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/product-"heat shock transcription factor"
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/clone="HSF-G1"
                                                                                                                                                                                                                  organism-"Schistosoma
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980 c 863 g
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/note="alternatively spliced HSF1 mRNA"
/product="heat shock transcription factor"
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/product="heat 
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/function="binds to HSE in promoters of Hsp genes"
/note="HSF2 protein; alternatively spliced product"
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NDGKYIYSLTGSSPECOVNTOSLVDKNEVNVQDGPFYLSKVDDNFTHFTNDEEEPVG
LNVEEDGVTDVNNSILENMPCSRSDTPYCLTDSPGLSDVIPSKLDGVEDSICDLL
NGDSQTEQEVCNNQPFSESTLSKYKKEPIRKQHKIQNEPRCIAPFAESDVDGFVSTTLQ
DIDSLPWEKYQDSGFDFNLDVEQNQTENSRSSSNGLIVGNEIIPVEPANLNACDDVIQ
FLRSEIPGKKLKSDEPLKTVATTEAHASTQNGAIDLTSSSSAPTTWKARLSANNRLTI
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FSESTLSKYKKEPIRKQHKIQNRPRCIAPFAESDPQFVSTTLQDIDSLPWEKYQDSGF
DFNLDVEQNQTENSRSSSNGLIVGNEIIPVEPANLNACDDVIQFLRSEIPGKKLKSDE
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IRNKDILLSKIQRRTSNMFSPJMGSRNQSEGYKVPYVQANSGLMGSISYSPQRPIPAF
DFLRLAETVRHLRCNQETLSQQISYLKSENQLLYRELSDLREHHDKQSQLIQTLFTFL
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DFLRLAETVRHLRCNQETLSQQISVLKSENQLLYRELSDLREHHDKQSQLIQTLFTFL
SAFAKEGRSASVCIGQTKRKALPSITPSGSRLQNKELKLDLRKGFQIERNSVQPLQLV
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/db_xref-"prote598"
/db_xref-"011:2895598"
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join(AF043419.1:963. .1073,AF043419
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/db_xref="PID:g2895599"
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                                                                                                                                                                                                        /protein_id="AAC39029.1
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                   1268 TTCTCAGAA 1276
33 ttctcagaa 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                     QTSDLLGSHKRPKFDIRNLSAKIGNTSSGANITDQISDIGSVVHILPSNLQLTPVSLG
NDECDVNTQSLVDKNPVNVQDGPRYYLSKVDDNFTHPTNDEEFPVGLNVEEDGVTDVN
NSILELNWPCSRSDTPYCLTDSPGLSDVIPSKLDGVTDESICDLLLNGDSQTEQEVGN
                                                                                                                                                                /number=10
666 c
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3232. .3580
                                                                                                                                                                                                                                    /number=8
2463. .2812
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1787. .1843
                                                                                                                                                                                                                                                                                                                                                               VLIRRQSITPLSTPDFCEEELE"
                                                                                                                                                                                                                                                                                                                                                                                  SDEPLKTVATTEAHASTQNGAIDLTSSSSAPTTWKARLSANNRLTISSSPKVKRKQVP
                                                                                                                                                                                                                                                                                                                                                                                                                      NQPFSESTLSKYKKEPIRKQHKIQNRPRCIAPFAESDPQFVSTTLQDIDSLPWEKYQD
                                                                                                                                                                                                                                                                                                            1590. .1747
                                                                                                                                                                                                                                                                                                                             'number=6
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                                                                                        Score 9; DB 22; 1
Pred. No. 8.17e+03;
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                                                                       Mismatches
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                                                                       0;
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3 (bases 1 to 3786)

3 (bases 1 to 3786)

2 veriov, V.V., Volkov, I.Y., Velikodvorskaya, T.V. and Schwarz, W.H.

Highly thermostable endo-1,3-beta-glucanase (laminarinase) LamA

from Thermotoga neapolitana: nucleotide sequence of the gene and

characterization of the recombinant gene product

Microbiology 143 (Pt 5), 1701-1708 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-JAN-1995) Zverlov V. V., genetics, Russian Academy of Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and expression in Escherichia coli of Thermotoga neapolitana genes coding for enzymes of carbohydrate sub
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Zverlov, V.V.
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Dakhova,O.N., Kurepina,N.E., Zverlov,V.V.,
Vellkodvorskaya,G.A.
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                                                                                                  /gene="bglB"
<1. .901
                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/strain-"z2706-MC24"
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                          /pseudo
                                                     /EC_number="3.2.1.21"
                                                                             /gene="bglB"
transl_table=11/
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FEATURES
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REFERENCE
AUTHORS
TITLE
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AUTHORS
                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
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ORIGIN
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                                                                               JOURNAL MEDLINE
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRATPEFHA 3820 bp DNA BCT 25-OCT-1993 Streptococcus faecalis F1F0 ATPase (atpE, atpF, atpH and atpA) genes, complete cds. M64265
                                                                                                                                                                                                                                                                                     Streptococcus faecalis (ATCC 9790) DNA.
Enterococcus faecalis
Eubacteria; Firmicutes; Low G+C gram-positive bacteria;
                                                                                                                                                                                                                                                                                                                                                            M64265.1 GI:153575
ATPase alpha subunit; ATPase beta subunit; ATPase delta subunit;
ATPase gamma subunit; F1F0-ATPase; H+-ATPase; atpA gene; atpE gene;
                                                                                                Shibata, C., Ehara, T., Tomura, K., Igarashi, K. and Kobayashi, H. Gene structure of Enterococcus hirae (Streptococcus faecalis) FIFO-ATPase, which functions as a regulator of cytoplasmic pH J. Bacteriol. 174, 6117-6124 (1992)
                                                                                                                                                                                                                           1 (bases 1
Kobayashi,H.
                                                                                                                                                                                                                                                                                                                                                 atpr gene; atpH gene.
                                                                                                                                                                                                   Unpublished (1991)
                                                                                                                                                                                                                                                                    Enterococcus.
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3864. 2883
"Jena" lama"
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Pred. No. 8.17e+03;
0; Mismatches 0;
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                                  h 100.0%;
Similarity 100.0%;
9; Conservative
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В

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1635. .3191
/gene="atpA"
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1070..1612
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NDYKGLLLGSYKTAVPLSDEGLQKLEMNVAKIMDYQTVELKQIVDSSIIGGAIVEANH
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/db_xref="PID:9153579"
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/db_xref-"PID:9153578"
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RESULT 200
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PN JP 1994189770-A/4

PD 12-JUL-1994

PF 31-MAY-1993 JP 1993128601

PF 31-MAY-1993 JP 1993128601

PF 01-JUN-1992 JP 92P 140706, 27-OCT-1992 JP 92P

SHINTANI ASAE, SASADA REIKO, IGARASHI KOICHI

PC C12N15/16,C12N15/63;

CC strandedness: Double;

CC topology: Linear;

CC Feature is identified by similarity;

FH Key Location/Qualifiers

FH Source /Organism-/Homo sapiens/

FT CDS 3276.3821

FT CDS 3276.3821
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A.thaliana phyD gene.
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The phytochrome apoprotein family in Arabidopsis is encoded by five genes: the sequences and expression of PHYD and PHYE
                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
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                              Clack, T., Mathews, S. and Sharrock, R.A.
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Location/Qualifiers
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SELGGRAMFVVVNACSSKDYLNNIVGYCFVGQDVTGHKIVMDKFINIQGDYKAIHSP
NPLIPPIFAADENTCCLEWNTAMEKLTGWPRSEVIGKLLVREVFGSYCRLKGPDALTK
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VRVVQDDRLTQFICLVGSTLRAPHGCHAQYMTNMGSIASLAMAVIINGNEEDGNGVNT
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                                                                                                                                                                                                                             /strain="Columbia"
/db_xref="taxon:3702"
/clone="lambda7151"
801 c 986 g
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WLVANHSDSTGLSTDSLGDAGYPRAAALGDAVCGMAVACITKRDFLFWFRSHTEKEIK
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LEFRMACAGEGVPPEKVQDMFHSSRWTSPEGLGLSVCRKILKLMNGGVQYIREFERSY
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LEPARTEDPALSIAGAVQSQKLAVRAISHLQSLPSGDIKLLCDTVVESVRDLTGYDRV
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/db_xref="taxon:3702"
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Search completed: Thu Oct 28 00:25:30 1999 .Job time : 369 secs.

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W09630515-A1. 03-OCT-1996; U04012. 25-MAR-1996; U04012. 27-MAR-1995; US-411020. (LIGA-) LIGAND PHARM INC. Liamb IP, Seidel HM, Tian Chan S; WPI; 96-45362/45. DNA construct for screening modulat transcription - contg. regulatory promoter operably linked to a heter Claim 5; Page 61; 72pp; English. A novel DNA construct comprises an a regulatory element having the pre to a promoter, which is operably li (preferably a marker gene). The ger	SULT T4158 T4158 04-JU Cytok Regul trans	ALIGNMENTS	198 9 100.0 1212 3 N40167 199 9 100.0 1218 49 V18169 200 9 100.0 1221 25 T42978	194 9 100.0 1185 29 102330 195 9 100.0 1189 49 V59981 196 9 100.0 1197 12 073730 197 9 100 0 1204 44 V37033	191 9 100.0 1180 60 V84163 192 9 100.0 1181 15 Q85933 193 9 100.0 1181 60 V84164	188 9 100.0 1163 14 Q81366 189 9 100.0 1167 46 V37401 190 9 100.0 1176 17 Q99950	185 9 100.0 1146 29 T66409 186 9 100.0 1146 57 V08935 187 9 100.0 1151 60 V55785	182 9 100.0 1112 3 021023 183 9 100.0 1119 42 V30002 184 9 100 0 1129 24 T29786	179 9 100.0 1097 47 V44860 180 9 100.0 1100 16 Q96139 181 9 100.0 1110 12 G72807	177 9 100.0 1087 47 T98694 177 9 100.0 1087 47 T98694 178 9 100.0 1092 38 T91592	174 9 100.0 1047 37 1051112 175 9 100.0 1060 10 0203112	172 9 100.0 1039 54 V08185 173 9 100.0 1044 38 V04889	170 9 100.0 1026 42 V23014 171 9 100.0 1039 54 V68168	168 9 100.0 1021 54 V69789	66 9 100.0 993 45 V24131 67 9 100.0 1016 28 T51349	164 9 100.0 972 30 T68932	162 9 100.0 958 39 T96064 163 9 100.0 961 14 Q79929	161 9 100.0 953 1 N91055	159 9 100.0 918 12 Q70200 159 9 100.0 918 12 Q70190 160 0 100 0 924 38 V06123	156 9 100.0 892 48 V32990 157 9 100.0 911 38 V06143
WO963 03-OC 03-OC 25-MF 27-MF 11GH 11GH 1 DNA C 1 trans Claim A nov a reg to a	SULT 1 141583 standard; DNA; 9 T41583; 04-JUN-1997 (first entr Cytokine activated STAT Regulatory element; prot transfection; agonist; a modulation; STAT; STAT5;	ALIGNMENTS	198 9 100.0 1212 33 199 9 100.0 1218 49 200 9 100.0 1221 25	194 9 100.0 1185 29 102330 195 9 100.0 1189 49 V59981 196 9 100.0 1197 12 073730 197 9 100 0 1204 44 V37033	191 9 100.0 1180 60 V84163 S 192 9 100.0 1181 15 085933 C 193 9 100.0 1181 60 V84164 S	188 9 100.0 1163 14 Q81366 Murine B lymphocyte 189 9 100.0 1167 46 V37401 Streptococcus pneum 190 9 100.0 1176 17 Q99950 Recombinant high as	185 9 100.0 1146 29 T66409 186 9 100.0 1146 57 V08935 187 9 100.0 1151 60 V55785	182 9 100.0 1112 3 Q21023 mg h 183 9 100.0 1119 42 V30002 DM 184 0 100 0 1119 42 V30002 DM 184 0 100 0 110 24 T30786 hMit	179 9 100.0 1097 47 V44860 180 9 100.0 1100 16 Q96139 181 9 100.0 1110 12 G72807	177 9 100.0 1087 47 177 9 100.0 1087 47 178 9 100.0 1092 38	174 9 100.0 1047 37 1051112 175 9 100.0 1060 10 0203112	172 9 100.0 1039 54 V08185 173 9 100.0 1044 38 V04889	170 9 100.0 1026 42 V23014 171 9 100.0 1039 54 V68168	168 9 100.0 1021 54 169 9 100.0 1022 18	66 9 100.0 993 45 V24131 67 9 100.0 1016 28 T51349	164 9 100.0 972 30 T68932 Bovine PIT-1 exon 6	162 9 100.0 958 39 T96064 Apo 163 9 100.0 961 14 Q79929 Ant	161 9 100.0 953 1 N91055 Seq	159 9 100.0 918 12 070190 Sequen	156 9 100.0 892 48 V32990 Human p24 vesicle 157 9 100.0 911 38 V05143 Viral infection ge

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                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 125; 135pp; English.

The present oligonucleotide comprises a regulatory element TT(Nx)AA, where x is 4-7, and the regulatory element binds an activated transcriptional regulatory protein in response to a signalling mol., i.e. a cytokine. This cytokine responsive DNA spacer regulatory element can be used to detect the presence of a transcriptional regulatory protein in a sample, and in assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sample
Claim 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine responsive DNA spacer regulatory element. Regulatory element: transcriptional regulatory protein; signalling molecule; DNA spacer; agonist; antagonist; a gene transcription; inflammation; cytopenia; cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T14149 standard; DNA; 9 BP T14149;
                            somatic gene therapy; Synthetic.
                                                                     Primer alpha(1)b for human alphoid DNA sequence. CENP-B box; mammalian artificial chromosome; MAC;
                                                                                                                                                                                                                                                                                                      ameliorate disease states caused by cytokine deficiency, e.g. inflammation, anaemia, cytopenia and (pre)cancerous conditions Sequence 9 BP; 3 A; 2 C; 1 G; 3 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA spacer regulatory elements responsive to cytokine(s) - detecting the presence of transcriptional regulatory protei
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WPI; 95-373797/48.
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10-APR-1995; U04477.
14-APR-1994; US-228935.
27-MAR-1995; US-410780.
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                                                         mammalian telomere; centromere; yeast
                                                                                                                   V24228 standard; DNA; 18 BP.
V24228;
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                                                                                                                                                                                                                                                                                                                                                 ranscriptional regulatory protein in a sample, and in ass
(ant)agonists of gene transcription. The identified cpds
be used to treat cytokine-induced disease states, or to
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Comparison of the invention. The construct is a mammalian contributed in the DNA construct of the invention. The construct is a mammalian contributed in the DNA construct of the invention. The construct is a mammalian contributed in the DNA construct, and comprises a mammalian telomere and a comprise in a mammalian telomere and a comprise in the CENP-B box sequence. The invention also relates to methods for the CENP-B box sequence. The method can be used to construct, modify conficiently in an introduced into mammalian cells. The MACs can be used to construct, modify can atably maintain YACs in yeast cells which have the ability to form CMACs when introduced into mammalian cells. The MACs can be used for basic studies on cryanisation and function of mammalian cells. The MACs can be used for basic studies on cryanisation and function of mammalian chromosomes and also as a vector to introduce DNA segments (genes) of interest to test their functions in the subject to variable expression due to integration position effect nor cause unpredictable insertion mutation on host chromosomes. Furthermore CMACs will have the capacity to accommodate a DNA segment up to megabases where an entire large gene or group of genes and regulatory elements could be included. The MACs can be used for somatic gene therapy or to construct transgenic mice.
PT DNA constructs containing cytokine-responsive regulatory elements -
PT useful in assays for transcription-regulating proteins or gene
PT transcription agonists or antagonists
PS Example 1; Column 19-20; 58pp; English.

CC V5882-V56976 and V61601-V61631 are oligonucleotides used in the
PS element linked to a promoter which is linked to a heterologous coding
CC element linked to a promoter which is linked to a heterologous coding
CC element linked to a promoter which is linked to a heterologous coding
CC element of that the coding sequence is under the transcriptional control
CC of the regulatory element and the promoter, where the regulatory element
CC of the regulatory element and TTCNNGAA, TTANYTAA, and TTCNYTAA
where N is A, T, C or G, and y = 3 or 4. The constructs can be used to
CC where N is A, T, C or G, and y = 3 or 4. The constructs can be used to
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(MASU/) MASUMOTO H.
(OKAZ/) OKAZARI T.
COOKE HJ, Grimes BR,
WPI; 98-216941/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIGA-) LIGAND PHARM INC.
Lamb IP, Seidel HM;
WPI; 98-541763/46.
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US5814517-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1998 (first entry)
Regulatory element containing oligonuclectide #101.
Cytokine-responsive regulatory; primer; promoter; detection; isolation; transcriptional control; STAT protein; screening; agonist; ss.
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26-AUG-1996; J02381.
26-AUG-1996; WO-J02381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V56942 standard; DNA; 19
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27-MAR-1995; US-410779.
14-APR-1994; US-228935.
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Similarity 100.0%;
9; Conservative
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18 BP; 3 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9;
Pred. No.
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. No. 1.37e+03;
Mismatches 0;
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PD 03-OCT-1996: U04012.

PF 25-MAR-1996; U5-411020.

PA (LIGA-) LIGAND PHARM INC.

PA (LIGA-) LIGAND PHARM INC.

PI Lamb IP, Seidel HM, Tian Chan S;

PI DRA construct for screening modulators of cytokine-mediated promoter operably linked to a heterologous gene promoter operably linked to a heterologous gene Seample 1; Page 26; 72pp; English.

CC A novel DNA construct comprises the present oligonucleotide (ON), CC which contains a core a regulatory element, operably linked to a cc promoter, which is operably linked to a heterologous gene CC (preferably a marker gene). The gene is under the transcriptional CC control of the promoter and the ON sequence when the ON is bound by CC a STAT protein activated in response to II-2, II-3, G-CSF, GM-CSF, CC II-13 or II-15. Cytokine responsive host cells transfected with the CNA construct can be used to measure the ability of a compound to act as an agonist or antagonist of cytokine mediated gene CC cytokine modulators involved in the STAT5 and/or STAT6 protein control of the protein in particular, they can be used to screen for cytokine modulators involved in the STAT5 and/or STAT6 protein
                                                                                                                                                                                                                                                                Query Match
Best Local :
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Best Local
                                                                                    Q91527;
Q91527;
22-DEC-1995 (first entry)
ETS-2 MspI RPLP primer.
Restriction fragment length polymorphism; RFLP; point mutation; mapping; primer; polymerase chain reaction; PCR; ETS-2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide containing core DNA regulatory element. Regulatory element: STAT; protein; cytokine; responsive; host cell; transfection; agonist; antagonist; mediated; STATS; transcription; modulation; signalling pathway; STAT6; oligonucleotide; electrophoretic mobility shift assay; EMSA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resulting complex. The cells can be used in screening assays for agonists of gene transcription, in which the level of expression of the coding sequence is measured in the presence and absence of a test compound or in the presence of the corresponding cytokine.

Sequence 19 BP; 6 A; 4 C; 5 G; 4 T;
                                                                                                                                                                                                                                                                                                                      signalling pathway. Following an electrophoretic mobility shift assay was found to bind IL-4 and IL-13 moderately. Sequence 19 BP; 4 A; 5 C; 4 G; 6 T;
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T41612;
T41612;
O4-JUN-1997 (first entry)
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                                                                                                      standard;
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Similarity 100.0%;
9; Conservative
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Similarity 100.0%;
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                                                                                                      DNA;
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Pred. No.
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Pred.
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1.37e+03
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PF 28-JUN-1990; JP-171986.

PR (SHIO) SHIONOGI KK.

PA (SHIO) SHIONOGI KK.

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Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local
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CA2136705-A.
27-MAY-1995.
25-NOV-1994; 136705.
26-NOV-1993; US-157269.
(CLAR-) CLARKE INST PSYCHIATRY.
Kennedy JL, Petronis A;
WPI; 95-255407/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q23061 standard; DNA; 20 BP.
Q23061;
Q23061;
31-JUI-1992 (first entry)
HPV-16 primer (2).
Primer; probe; PCR; amplification; cervical cancer; condyloma;
Powen's disease; verruca; oral cavity cancer; pharynx cancer;
Laryngeal cancer; detection; ss.
Human papilloma virus.
J04058888-A.
Z5-FEB-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for polymorphism by amplification of pooled nucleic acid - restriction with endonuclease(s), sepn. of fragments and comparison of restriction patterns, for detecting disease related mutation(s), in genetic mapping etc.

Example 5; Page 33; 48pp; English.

The primers given in Q91526-27 were used for the analysis of the ETS-2 MspI PCR-RFIP. Restriction patterns of PCR products were compared to detect the polymorphism.

Sequence 20 BP; 6 A; 2 C; 6 G; 6 T;
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                                                                                                                                                                 25 ttctgagaa 33
                                                                                                                                                                                                          4 ttctgagaa
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                                                                                                                                                                                                                                                        Score 9;
Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                   9; DB 3; L
No. 1.37e+03
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1.37e+03;
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T88330; standard; DNA; 20 BP. T88330; T22-MAY-1998 (first entry) Primer E2-A for murine DP-3 protein E region cDNA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PT New DNA encoding human phosphomannomutase or its fragments - used to produce the nutations associated with carbohydrate-deficient glycoprotein produced syndrome-1, particularly for prenatal diagnosis ps Disclosure; Fig 3-6; 104pp; English.

CC The invention relates to a human phosphomannomutase-2 (PMM2) protein and CC the nucleotide sequence encoding the protein. The DNA or its fragments care used to detect mutation in the PMM2 genes that are associated with CC sequences can also be used to detect expression of PMM2-related cDNA; to CC express PMM2 or its mutants; and to create transgenic animals for use in CC drug screening and for studying expression pathways. The expressed CC proteins are used to screen for agents that modulate activity of PMM2, for therapy and to raise specific antibodies (for detecting PMM2 or its mutants, in competitive or capture assays). Blochemical assays for CC cutants, in competitive or capture assays). Blochemical assays for CC phophomannomutase activity are used to identify possible carriers of CDG1 (Jaeken disease). Measuring enzymatic activity in foetal cells (or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches
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The present sequence was used in the development of a novel assay for a putative regulator of cell cycle progression. The assay comprises expressing in a cell a protein comprising the E region and sufficient C-terminal residues of a DP-3 protein to provide a functional nuclear localisation signal (NLS), or the NLS of E2F-1, and a marker for nuclear localisation. Then the degree of nuclear localisation. Then the degree of nuclear localisation in the presence and absence of the putative regulator is determined. Regulators identified using the assay can be used as potential regulators of cell proliferation, or as models for rational drug design. Regulation of the NLS may lead to effects such as enhanced cell division, blocking of cell cycle progression or apoptosis. The regulators may also be used to design other
                                                                                                                                                                                                                                                                                                                                             05-NOV-1998.
30-APR-1998; E02593.
27-JAN-19998; GB-001719.
30-APR-1997; GB-008851.
(GENZ ) GENZYME UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
Mus sp.
W09743647-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-1999 (first entry)
Human PMM2 intron 5/exon 6 junction sequence.
Phosphomannomutase-2; PMM2; CDG1; mutation; human;
carbohydrate-deficient glycoprotein syndrome type 1
Jaeken disease; prenatal diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assaying; cell cycle nuclear localisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assays for identifying regulators of cell cycle progression comprise expressing a protein having a transcription factor localisation signal and determining the degree of nuclear
                                                                                                                                                                                                                                                                                                          Matthijs G;
WPI; 99-024063/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V80051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-1996; GB-010195.
(MEDI:) MEDICAL RES COUNCIL.
De La Luna S, La Thangue NB;
WPI; 98-009053/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
WO9849324-A2.
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15-MAY-1997; G01324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA;
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Similarity 100.0%;
9; Conservative
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7 A; 3 C;
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signal; NLS;
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Pred. No.
0; Misma
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mouse; murine; PCR pr
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1.37e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; transgenic; assay;
1; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
     carriers of CDG1 cells (or in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of polynucleotides with desired properties - by iterative presentation and recombination products were used to introduce mutations into the TEM-1 pck primars V54900-14 were used to introduce mutations into the TEM-1 betalactamase gene. The PCR products were used to construct muatnt combinantions of the gene, using the method of the invention. The specification describes a method for evolving a polynucleotide for acquisition of a desired property. The method comprises providing a population of variants of the polynucleotide, at least one of which is in cell-iree form, shuffling the variants of the polynucleotide to form recombinant polynucleotides, selecting or screening for recombinant colynucleotides, selecting or screening for recombinant polynucleotide have evolved toward the desired property and repeating the steps with the selected recombinant polynucleotide has acquired the desired property. The recombinant polynucleotide has acquired the desired property. The can be formulated as a pharmaceutical.

So sequence 22 BP; 8 A; 4 C; 3 G; 7 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches
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Best Local Similarity 100.0%;
Matches 9; Conservative
                            18-NOV-1996;
16-NOV-1995;
27-FEB-1996;
21-OCT-1996;
                                                                                                                                                                                                                                16-SEP-1997 (first entry)
PIK-related kinase MCGS1 PCR primer oDH26.
Mammalian cell cycle surveillance 1 beta; MCCS1 beta;
PIK-related kinase; phosphatidylinositol kinase; DNA;
RIK-related kinase; phosphatidylinositol kinase; DNA;
RIK-related kinase; polymerase chain reaction; PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parental leucocytes if such cells are unavailable) and detecting mutations in the PMM2 gene makes possible a better prenatal diagnosis CDG1. Sequences V80046-60 represent PMM2 exon/intron junction sequence sequence 20 BP; 9 A; 2 C; 2 G; 7 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crameri A, Stemmer WPC; WPI; 98-530860/45.
Production of polynucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-1998.
30-NOV-1995; 564955.
04-MAR-1996; US-537874.
17-FEB-1994; US-198431.
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                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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to introduce E104K mutation into TEM-1 betalactamase gene.
totamase gene; recombination; gene shuffling; PCR primer; second intercombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
larity 100.0%;
Conservative
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Pred.
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0; M
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1. No. 1.37e+03;
Mismatches 0;
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No. 1.37e+03;
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                                                                                                                                                                                                                                            primer;
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US-558666. US-007312. US-725304.

Hoekstra WPI; 97-2

stra MF, Holtzman 97-289299/26.

DA,

Keegan

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Phosphatidylinositol kinase-related mammalian

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                                                                                                            Š
                                                                                                                                 PT New isolated nucleic acid segments from the human genome - used for pridetermining polymorphic forms for use in e.g. forensics, paternity pri testing or phenotypic typing for disease ps. Claim 16; Page 202; 310pp; English.

Claim 16; Page 202; 310pp; English.

CC sucolation of various biallelic polymorphic markers found in the human cc genome (represented in x10269-x12937). These primers can be used in a genome (represented in x10269-x12937). These primers can be used in a cc forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial cc hypercholesterolemia, polycystic kidney disease, hereditary hypercholesterolemia, polycystic kidney disease, hereditary chaemorrhegic telangiectasia, familial colonic polyposis, bheres Danlos conditions, osteogenesis imperfecta, acute intermittent porphyria, caucinamune diseases inflammation, cancer, diseases of the nervous creation by pathogenic microorganisms, and characteristics such cas longevity, appearance (e.g. baldness, obesity), strength, speed, cendurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid cagments can also be used to produce medicaments for the treatment or recombinates of such diseases.
                                  Query Match
Best Local S
Matches
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Best Local S
Matches
                                                                                                         prophylaxis
Sequence 2
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Primers oDH23 (T72674) and oDH26 (T72679) were used to amplify a portion of the human mammalian cell cycle surveillance 1 (MCCS1) gene. Primer oDH26 is based on the MCCS1 alpha cDNA sequence (see also T72664). The primers were used in a PCR-based assay to map the MCCS1 gene to human chromosome 3. A 237 bp product was generated from a human/rodent chromosome 3 hybrid. In a second set of amplification reactions, the same primers were used to sublocalise the MCCS1 gene to the interval between q21 and q25.1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1997; U20313.

06-NOV-1996; US-0304455.

(WHED) WHITEHEAD INST BIOMEDICAL RES

Hudson T, Lander ES, Wang D;

WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human biallelic polymorphic marker downstream primer #427.

Human biallelic polymorphic marker downstream primer #427.

Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X10121
X10121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment; marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-1999 (first entry)
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25 ttctgagaa 33
ttctcagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                  h 100.0% Similarity 100.0% 9; Conservative
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Similarity 100.0%;
9; Conservative
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                                                                                                          of such diseases.
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C;
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C;
                                  re 9; DB 59; I
1. No. 1.37e+03;
Mismatches 0
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. No. 1.37e+03;
Mismatches 0;
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RESULT IN RESULT
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DE19627031-A1.

09-JAN-1997.

04-JUL-1996; 027031.

04-JUL-1995; DE-024347.

04-JUL-1995; DE-024346.

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                        W09705278-A1.
13-FEB-1997.
24-JUL-1996; G01794.
12-DEC-1995; GB-025364.
27-JUL-1995; GB-015385.
(DALG-) DALGETY PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting antibodies against human papilloma virus proteins - for early diagnosis of HPV-mediated carcinoma

Example 1; Page 4; Spp; German.

Methods for detecting antibodies directed specifically against human papilloma virus (HPV) proteins are claimed. In particular, the method is used to detect uncontrolled expression of the HPV E6 and E7 genes to provide early diagnosis of HPV-associated cancers, especially cervical and oral carcinoma. A HPV protein is bound to a carrier and is then incubated with a sample such that any anti-HPV antibodies become bound. The immobilised antibodies are detected, either directly or indirectly, by reaction with an anti-idiotype antibody. In a specific example, the HPV 16 E7 protein was fused to a C-terminal sequence of 11 amino acids from the SV40 T antigen for immobilisation.
                                                                                                                                                                                                                                                                         Wales R
WPI; 97
Primers IFN-beta REVERSE (T84431) and IFN-beta CRC FORWARD (T84432) are based on the pig interferon-beta (IFN-beta) gene. They can be utilised in an internal standard PCR amplification of pig genomic DNA, simulataneously with primers (see T84420-27) specific for the pig KIT gene. DNA amplified from pig genomic DNA by the KIT gene
                                                                                                                                            Determn. of coat colour genotype in pigs by analysis for duplication or deletions, or analysis of KIT prestablish breeding programmes for pigs of selected coclaim 12; Page 39; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interferon-beta gene reverse primer for standard PCR. KIT gene; pig; coat colour; pigmentation; primer; PCR; polymerase chain reaction; interferon-beta; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TR4431 standard; DNA; 26 BI
TR4431;
TR4431;
13-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Braspenning J, Frey
Velhagen I, Zentgraf
WPI; 97-066767/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-1997 (first entry)
Human papilloma virus 16 E7 gene PCR primer.
HPV16; E7 protein; fusion protein; oral carc
polymerase chain reaction; immunodetection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T59391 standard; DNA; T59391;
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Sequence 24 BP; 5 A; 4 C; 6 G; 9 T;
                                                                                                                                                                                                                                                                                                                            Andersson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ű
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Pred. No. 1.37e+03
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Best Local S
Matches
                                                                 Query Match
Best Local Similarity 100.0%;
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29-JAN-1993: U00977.
29-JAN-1992: US-827208.
29-MAR-1992: US-857059.
12-NOV-1992: US-974409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quantitating messenger RNA in sample - using immobilised-poly-
Claim 15 and 38; Page 46; 177pp; English.

The sequences given in Q47433-44 are primers which were used in the quantification of human GTP binding protein (G protein)-specific mRNAs. These primers are derived from human and rat G-protein sequences. These primers were used in conjunction with the method of the invention, in PCR, for the detection and quantification of mRNAs in a sample without the need to purify the mRNA from cells. The claimed method comprises identifying a polynucleotide sequence unique to the mRNA, and immobilising an oligomer complementary to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primers is quantitated by comparison to DNA amplified using the IFN-beta primers. The 3 alleles for pig coat colour (I, inhibition of coat colour; I(p), patch; and i, development of colour) can be differentiated on the basis of duplication/deletion in the KIT gene. This allows breeding of pigs with the desired, usually white, coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HITB ) HITACHI CHEM CO LTD. (HITB ) HITACHI CHEM RES CENT INC. Akitaya T, Cooper A, Mitsuhashi M; WPI; 93-258695/32.
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alpha subunit; specific mRNA; detection; hybridisation; dispnosis;
pathophysiology; disease state; hereditary: cancer; infectious;
osteodystrophy; pituitary tumour; acromegaly; melanoma cells;
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Local Similarity 100.0%;
nes 9; Conservative
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CC the sequences given in Q47445-51 are probes which were used in the CC quantification of human GTP binding protein (G protein) specific CC mRNAs. These probes are derived from human and rat G-protein CC sequences. These probes were used in the method of the invention, CC for the detection and quantification of mRNAs in a sample without CC immobilising an oligomer complementary to this sequence to an CC insoluble support. The sample is then incubated with the insoluble coligomer and be immobilised. Non-immobilised components are washed CC from the support and bound RNA is labelled in such a way that the CC label is incorporated onto the support relative to the amount of CC mRNA on the support. The amount of bound label is then determined. CC mRNA on the support. The amount of bound label is then determined. CC diagnosing and recognition of pathophysiology of various disease states, eg. hereditary diseases, cancer, and infectious diseases. CC groteins are thought to be involved in causing various diseases convolved in invasive and metastatic melanoma cells, and diabetes. Seminor CC Seminor CC observation and metastatic melanoma cells, and diabetes.

CC Seminor CC Semin
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29-JAN-1993; U00977.
29-JAN-1992; US-827208.
24-MAR-1992; US-857059.
12-NOV-1992; US-974409.
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                      V70065;
01-MAR-1999 (first entry)
Human SSX1 gene-specific PCR primer SSX 1B(3').
SSX1; SSX gene; human; tumour associated antige
PCR; primer; ss.
Synthetic.
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(HITB ) HITACHI CHEM RES CENT INC.
Akitaya T. Cooper A, mitsuhashi M;
WPI; 93-258695/32.
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                                                                                                   associated antigen;
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d. No. 1.37e+03;
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PS Example 5; Page 47; 177p; English.

PS Example 6; Page 47; 177p; English.

PS Example 7; Page 47; 177p; English.

PS Example 6; Page 47; 177p; English.

PS Example 7; Page 47; 177p; English.

PS Example 6; Page 47; 177p; English.

PS Example 7; Page 47; 177p;
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Best Local S
Matches
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29-JAN-1993; US-827208.
29-JAN-1992; US-827208.
24-MAR-1992; US-957059.
12-NOV-1992; US-974409.
(HITB ) HITACHI CHEM CO LTD.
(HITB ) HITACHI CHEM RES CENT INC.
Akitaya T, Cooper A, Mitsuhashi M;
WPI: 93-258695/32.
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05-MAY-1997; US-651138.
(LUDW-) LUDWIG INST CANCER RES.
Chen Y, Gure AO, Knuth A, Old LJ
Sahin U, Scanlan MJ, Tsang S, Tu
WPI; 98-610379/51.
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G protein, Gi-1
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This is the nucleotide sequence of primer SSX 1B(3'), which corresponds to nucleotides 440-465 of the human SSX1 gene. It is used with primer SSX 1A(5') (see V70064) in PCR amplifications in order to determine expression of the SSX1 gene in normal and tumour tissues. Gene-specific primer pairs (see V70064-73) are provided for SSX genes 1-5. Determination of SSX gene expression provides a means for assaying for cancers such as melanoma.

Sequence 26 BP; 9 A; 5 C; 2 G; 10 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probe; quantification; human; GTP binding protein; G protein;
alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
pathophysiology; disease state; hereditary; cancer; infectious;
osteodystrophy; pituitary tumour; acromegaly; melanoma cells;
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Q47445 standard;
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Pred. No. 1.37e+03;
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                                                                                                                                                                   PT Quantification gessenger RNA in sample - using immobilised poly-
PS Claim 14 and 38; Page 47, 177pp; English.

CC The sequences given in Q47445-51 are probes which were used in the
CC quantification of human GTP binding protein (G protein) specific
CC mRNAs. These probes are derived from human and rat G-protein
CC sequences. These probes were used in the method of the invention,
CC for the detection and quantification of mRNAs in a sample without
CC the need to purify the mRNA from cells. The claimed method comprises
CC identifying a polynuclectide sequence unique to the mRNA, and
CC inmobilising an oilgomer complementary to this sequence to an
CC ingomer and be immobilised. Non-immobilised components are washed
CC oligomer and be immobilised. Non-immobilised components are washed
CC from the support and bound RNA is labelled in such a way that the
CC label is incorporated onto the support relative to the amount of
CC diagnosing and recognition of pathophysiology of various disease.
CC quantification of multiple varieties of mRNA. It may be used for
CC diagnosing and recognition of pathophysiology of various disease.
CC states. A genetic deficiency of Gs protein is the molecular basis of
CC hereditary osteodystrophy. Pliuitary tumours in acromegalic patients
CC have been shown to contain mutant Gs proteins. G proteins are also
CC clovolved in invasive and metastatic melanomer cells, and diabetes.
CC See also 047381-666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ဌ
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Probe; quantification; human; GTP binding protein; G protein; alpha subunit; specific mRNA; detection; hybridisation; diagn pathophysiology; disease state; hereditary; cancer; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hereditary osteodystrophy. Pituitary tumours in have been shown to contain mutant Gs proteins. (involved in invasive and metastatic melanoma cell See also Q47381-666.

Sequence 26 BP; 10 A; 4 C; 6 G; 6 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HITB ) HITACHI CHEM CO LTD.

(HITB ) HITACHI CHEM RES CENT INC.

(Akitaya T. Cooper A, Mitsuhashi M;

WPI: 93-258695/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1993; U00977.
29-JAN-1992; US-827208.
24-MAR-1992; US-857059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
nucleotide havi nucleotide having sequence complementary to sequence unique the mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathophysiology;
osteodystrophy; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q47451 standard; cDNA to m
Q47451;
26-JAN-1994 (first entry)
Human G protein, Gi-1, pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09315221-A.
05-AUG-1993.
                                                                                                                                                             See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dlabetes; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1992; US-974409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                     Local Similarity
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                                                                                                                                                      in invasive and metastatic Q47381-666.
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larity 100.0%;
Conservative
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      Score 9;
Pred. No.
0; Misma
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Pred.
0; M
                                                                                                                             4 C;
      re 9; DB 7; Leu
1. No. 1.37e+03;
Mismatches 0
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. No. 1.37e+03;
Mismatches 0;
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                                                              Length 26;
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PT Amplification and detection of target nucleic acid sequences - PT comprises chemical linkage of oligo:nucleotide probe complement PT pairs, esp. useful for detecting single point mutation(s) pairs, esp. useful for detecting single point mutation(s) PS Example 1; Page 62; 128pp; English.

CC The sequences given in T43146-49 represent probes which were used in the Aman CC papilloma virus (HPV) type 16 genome using the method of the invention.

CC The method uses two oligonucleotide probe complement pairs (OPCPs). Each CC member of the probe pair contains a chemical functionality group which come another following hybridisation of the probe pairs to the tengent of the probe in each OPCP is composed of two regions; the first region hybridises to the target and contains the chemical functionality group while the second region prevents target independent joining. The CC other probe in the OPCP contains the corresponding chemical functionality group while the second region prevents target independent joining. The CC other probe pairs in a OPCP are joined, they can serve as template CC for the second OPCP, which can in turn serve as template for unjoined CC first probe pairs in a cyclic amplification process. The method provides of sequences. It can identify minute sequence alterations in genes such as point mutations. The method can be used for the diagnosts of specific CC disease or testing of susceptibility to diseases such as autoimune to classification and sectorm. paternity testing, forensic conserve the content of the presence of t
                                                                                                                                                                                        Matches
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07-NOV-1996.
30-APR-1996; U
  LT 21
T30487 standard;
T30487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Segev
WPI; 9
                                                                                                                                                                                                                                                                         diseases or cancers. It can also be used for identifying the presence of a foreign genetic sequence e.g. for detecting specific bacterial or viral sequences in plant or animal samples.

Sequence 27 BP; 5 A; 9 C; 5 G; 7 T; 1 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe; amplification; detection; Human Papilloma virus; HPV; type 16; oligonucleotide probe complement pair; OPCP; hybridisation; cancer; non-enzymatic; point mutation; diagnosis; blood typing; dentification; tissue classification-HLA-typing; sex determination; paternity testing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUL-1997 (first entry)
HPV type 16 detection probe 2'.
Probe; amplification; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T43149 standard;
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                                                                                                        ttctcagaa
                                                                                                                                             ttctcagaa
                                                                                                                                                                                                        Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-431527.
RAD LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U06042
                                                                                                                                                                                        Conservative
                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "Modified by a chemical functionality group attached to a substituent group of the uridine residue, preferably attached to the C2' position of the ribose motety uridine, serves as a dienophile in the Diels Alder reaction between this group and the modification of T43148"
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"Targeting sequence
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Example; Page 39; 75pp; English.

CC T30459-T30545 represent amplification primers for the coding sequences CC for the variable chains of an antibody produced by the hybridoma cell Cline HNK-20. T30464-T30498 represent amplification primers for the coding sequence for the variable kappa chain of the HNK-20 antibody. CC HNK-20 is a murine hybridoma cell line, that produces IgA specific for CC the F glycoprotein of respiratory syncytial virus (RSV). The variable specific for the 5' untranslated region of the variable region, and for CC the intron downstream of the rearranged J region. The amplified CC sequences can be inserted into vectors containing heterologous (such as CC human) constant region genes, for the production of chimeric and cC can didagnosis of infection by RSV, such as pneumonia and bronchiolitis, CC and diagnosis of infection by RSV, such as a template, variable region genes can be isolated without producing fragments that have to be a contained for recombinant antibody expression. Also, by using the genomic CC base, no knowledge of the DNA sequence encoding the target variable region can recombine contained contained from the encoded morefules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              HPV type 16 detection probe 2.

Probe; amplification; detection; Human Papilloma virus; HPV; type 16; oligonucleotide probe complement pair; OPCP; hybridisation; cancer: non-enzymatic; point mutation; diagnosis; blood typing; identification; tissue classification-HLA-typing; sex determination; paternity testing;
   W09634984-A1
                                                                                                                                                                                                                                          modified_base
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 22
T43147 standard;
                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is required. Chimeric antibodies produced from the that contain the constant region of the host being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berdoz J, Kraeher
WPI; 96-286826/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                            forensic
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Local Similarity 100.0%;
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttctcagaa
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ORAVAX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                            science;
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                            /note- "Modified by a chemical functionality group attached to a substituent group of the uridine residue, preferably attached to the C2' position of the ribose molety uridine, serves as a dienophile in the Diels Alder reaction between this group and the modification of T43146"
                                                                                                                                                                                                                                          /note=
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                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 1..29
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                                                                                                                                                                                                                                                                   "Targeting sequence
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Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
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CC The sequences given in T4316-49 represent probes which were used in the CC amplification and detection of a 54 by sequence contained in the Human CC papilloma virus (HPV) type 16 genome using the method of the invention. CC The method uses two ollgonucleotide probe complement pairs (OPCPs). Each CC permits linkage of the probes when the functionality groups are adjacent to one another following hybridisation of the probe pairs to the cemplate. One probe in each OPCP is composed of two regions; the first cregion hybridises to the target and contains the chemical functionality group while the second region prevents target independent joining. The CC group while the second region prevents target independent joining. The CC group while the second opcp, which can in turn serve as template for unjoined CC group. When two probes in a OPCP are joined, they can serve as template for the non-enzymatic amplification process. The method provides for the non-enzymatic amplification process. The method provides CC first probe pairs in a cyclic amplification process. The method provides GC for the non-enzymatic amplification and detection of target nucleic acid sequences. It can identify minute sequence alterations in genes such as conditional process if cation-HAr-typing, sex determin, paternity testing, forensic CC diseases or cancers. It can also be used for the diagnosis of specific CC diseases or cancers. It can also be used for identifying the presence of trail sequences in plant or animal samples.

Sequence 29 BP; 9 A; 5 C; 9 G; 5 T; 1 U;
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                                               PD 09-CAN-1995; DE-024347.

PF 04-JUL-1995; DE-024347.

PR 04-JUL-1995; DE-024346.

PR
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Human papilloma virus 16 E7 gene PCR primer.
HPV16; E7 protein; fusion protein; oral carcinoma;
polymerase chain reaction; immunodetection; ss.
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T59395 standard; DNA;
T59395;
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Amplification and
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30-APR-1996; U06042.
01-MAY-1995; US-431527.
(BIRA ) BIO-RAD LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE19627031-A1.
                                decreasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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Similarity 100.0%;
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     urea content.
32 BP; 9 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred.
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        10 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 30; Ld
1.37e+03;
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        10
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DR WPI; 98-28697/25.

PT bal bacterial promoter for increasing expression of heterologous prolypeptide - containing components of tac and gal promoters, especially for producing enzymes for oligosaccharide synthesis propertially for producing enzymes for oligosaccharide synthesis process for oligosaccharide synthesis promoter from the UDPgalactose of the containing the tac promoter from the UDPgalactose-4-epimerase constitutes for the promoter was designed to hybridise to contain the promoter was designed to hybridise to contain the promoter on pHP1/tac, while the 3 for promoter was designed to hybridise to a sequenced region of the galf promoter was designed to hybridise to a sequenced region of the galf constitutes which encompassed both the tac and galf promoters (see CC v31431), was inserted into pPHOX2. The invention provides novel coperably linked to a heterologous nucleic acid which encodes a compassed both the cacid which encodes a cacid which encodes a cacid which encodes a cacid which
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Best Local S
Matches
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Best Local (
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                                    22-MAR-1995.

19-MAY-1994; 112172.

19-MAY-1994; CN-112172.

(UYFU-) UNIV FUDAN.

Cai W, Li C, Zhao S;

WFI; 97-245915/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-1998 (first entry)
Dual tac-gal promoter 3' PCR primer.
Vector; dual promoter; tac promoter; galE promoter;
UDDgalactose 4-epimerase; plasmid pTGK; PCR; primer;
Synthetic.
                                                                                                                                                                                                                     01-JUN-1998 (first entry)
Primer #2 to amplify hTNF-alpha-Da construct.
Primer; PCR; amplification; human tumour necrosis factor-alpha; E. colhrnF-alpha; extracellular domain; deletion mutant; expression vector;
                                                                                                                                                                                                                                                                                                             V05901
                                                                                                                                                                  Homo sapiens.
CN1100464-A.
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Hermanson G, Schultz J;
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V31436 standard; DNA; 32
  Human tumor necrosin & Claim 2; Page 2; 11pp;
                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1997; U20528.
08-NOV-1996; US-029545.
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Similarity 100.0%;
9; Conservative
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Similarity 100.0%;
9; Conservative
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  derivative and its preparing Chinese.
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Pred. No.
0; Misma
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Pred. No. 1.37e+03;
0; Mismatches 0;
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1.37e+03
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TRESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pr to develop products for the detection of M. tuberculosis infection products for diagnosis, treatment and prevention of tuberculosis infection ccc protein containing the immunogenic polypeptides ThRa3, 38kD and Tb38-1 CC from Mycobacterium tuberculosis (MT). This fusion protein can be used in cca method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be sequence 33 BP; 11 A; 7 C; 9 G; 6 T.
            RESULT
AC V.
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13-MAR-1997; US-818112.
11-OCT-1996; US-730510.
(CORI-) CORIXA CORP.
Campos-Neto A, Dillon DC, H
13-NOV-1997.
07-MAY-1997; U07625.
08-MAY-1996; US-646538.
(USSH) US SEC DEPT HEALTH.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Gaitanaris GA, Pavlakis GN, Stauber RH,
                                                                                                                                                                                                                                                                                                                     Green fluorescent
genetic engineerin
Synthetic
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                     19-MAY 1998 (first entry)
19-MAY 1998 (first entry)
Primer Bio52 for green fluorescent protein coding sequence.
Green fluorescent protein; GFP; blue fluorescent protein; BFP;
genetic engineering marker; gene therapy; PCR primer; amplify;
                                                                                                                                                                                                                                         Aequorea victoria.
WO9742320-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9816646-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 34 BP.
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Similarity 100.0%;
9; Conservative
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osis; immunogenic; soluble; antigen; protective immunity;
pharmaceutical; infection; diagnosis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
larity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houghton R, Lodes MJ,
dzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 9;
Pred. No.
0; Misma
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Pred. No.
0; Misma
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. 1.37e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 52; I
1.37e+03;
                    Vournakis
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                    ű,
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38kD and Tb38-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                             jellyfish;
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transformation, subcellular localisation of proteins, for assessing proteins formation, subcellular localisation of proteins, for assessing protein that the protein (GFP) of Aequorea victoria. The amplified sequence is mutated to produce the nucleic acid of the invention that encodes a composed that is (a) a protein that has Leu at position 65 (and optionally further Cys at 66) and has cellular composed to the sequence at least 5 times that of wild-type GFP or (b) is a blue of Leu at 65 and Ala at 164, and has cellular fluorescence at least 5 (composed that of BFP (Tyr67 to His). The nucleic acids can be used as composed that of BFP (Tyr67 to His). The nucleic acids can be used to detect and characterise regulatory and coding sequence elements that composed to subcellular expression and targeting of proteins. Typical control subcellular expression and targeting of proteins. Typical control of a promoter induced by a particular analyte); assessment of compounds; and for drug screening (where expression is controlled by the promoter of a target gene), particularly for antiviral cor antiparasitic agents.

Sequence 34 BP; 12 A; 8 C; 9 G; 5 T;
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Best Local
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                                                                                                                         Claim 13; Page 10; 31pp; English.

Primer L126N is one of several primers which are preferred for in amplifying inter-repeat regions of DNA. The amplified fra are subjected to 2-D electrophoresis on the basis of length differences in base sequence. The resulting separation patter transferred to a filter for screening with a probe. The method be used to detect genetic variation.

See Q27389-Q27404 and Q33141-Q33144.

Sequence 34 BP; 9 A; 11 C; 11 G; 3 T;
                                                                                                                                                                                                                                                     on fragmen
PCR.
Claim 13;
                                                                                                                                                                                                                                                                                   Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried on fragments consisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                              06-AUG-1992.
24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
(INGE-) INGENY BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1993 (first entry)
Human chromosome 21 centromere-specific L1.26 primer L126N.
Polymerase chain reaction; PCR; repetitive element;
Kpn family; Alu-like repeat family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 97-558982/51.
New nucleic acid encodi
increased fluorescence
                                                                                                                                                                                                                                                                                                                                  WPI; 92-284683/34.
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                               24 ttctcagaa
                                                                              Local Similarity
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   ttctcagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA;
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Similarity 100.0%;
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                                                             Score 9;
Pred. No.
0; Misn
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Pred. No.
0; Misma
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. 1.37e+03;
                                                                              DB 4;
1.37e
                                                                               37e+03
                                                                                              Length
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                                                                                                                                                                           method
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N W030318/-A.

PD 18-FEB-1993:

PF 28-UUL-1992: U06617.

PR 31-UUL-1991: US-738800.

PA (STAD ) AMOCO CORP.

PO MCCIcle acid probes for detection of shigella and other pathogens per used to diagnose dysentery in non-isotopic test format and have utility in non-isotopic test formats requiring amplification for per high sensitivity

PS Claim 35: Page 99; L39pp; English.

CC The sequences given in 037534-45 are probes which was derived from Shigella specific fragment NT11-2. These probes substantially retain CC the exclusivity behaviour of NT11-2 towards non-enteroinvasive E. coli (EIEC) Enterobacteriaceae. Probes such as this one can be used in the detaction of dysentry causing microbes. See also 037506-35.
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ACCOMENTATION
ACCOMENTA
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Matches
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Shigella probe 1683.
Chromosome; Shigella; sonnei; flexneri; probe; Enteroinvasive; EIEC;
E. coli; transposable element; virulence plasmid; detection; dysentry;
NT11-2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
WO9633207-A1.
24-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide amplification using bivalent PCR primer to generate rolling circle intermediate or linear concatemers - requires reduce amt. of primer compared to conventional PCR example 2; Fig SA; 77pp; English.

The present sequence is a component oligonucleotide of the 2.71 kb plasmid pl85fil (Stemmer (1994) Nature 370:389), which encodes the gene and promoter region for R-TEM1 beta-lactamase. A collection of 134 component oligonucleotides, including the present sequence, were synthesised and used to assemble the plasmid by end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid p1825fil component oligonucleotide R18. 
Oligonucleotide; plasmid; p1825fil; gene; promoter; 
beta-lactamase; construction; assembly; synthesis; 
complementary; polymerase; reaction; ECPR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
WO9303187-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementary polymerase reaction (ECPR), employing the overlapping ends of the oilgonucleotides.
Sequence 40 BP; 11 A; 10 C; 10 G; 9 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-1996; U05480.
18-APR-1995; US-425684.
(GLAX ) GLAXO GROUP LTD.
Lipshutz RJ, Stemmer WPC;
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T69419 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q37535 standard; DNA; 41 BP
Q37535;
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                                       ttctgagaa
|}||||||||
   ttctgagaa 33
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Similarity 100
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larity 100.0%;
Conservative
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                                                                                                                                                    Conservative
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d. No. 1.37e+03;
Mismatches 0
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                                                                                                                                                                                               37e+03
                                                                                                                                                                                                                      Length 41;
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So Sequence 42 BP; 14 A; 9 C; 7 G; 12 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-NOV-1998 (first entry)
Primer used to introduce E104K
TEM-1 betalactamase gene; recon
Synthetic.
US5811238-A.
22-SEP-1998.
30-NOV-1995; 564955.
04-MAR-1996; US-537874.
17-FEB-1994; US-198431.
17-FEB-1994; US-198431.
30-NOV-1995; US-564955.
(AFFY-) AFFYMAX TECHNOLOGIES NV
Crameri A, Stemmer WPC;
WPI; 98-530860/45.
                                                                                                                                                                              Synthetic.

W09720078-A1.

05-JUN-1997.

02-DEC-1996; U19256.

02-DEC-1996; US-621859.

25-MAR-1996; US-564955.

30-NCV-1995; US-564955.

30-NCV-1996; US-564958.

(AFFY-) AFFYMAX TECHNOLOGIES NOT Crameri A, Stemmer WPC;

WPI; 97-310628/28.
green fluorescent protein

Example 6; Page 121; 209pp; English.

Mutagenic PCR primers T73029-43 were used to amplify the TEM-1
betalactamase gene, and introduce mutations into it. The present prim
introduces the amino acid change Glul04Lys. The TEM-1 betalactamase g
confers resistance to bacteria against approximately 0.02 micrograms
the drug cefotaxime. TEM-1 betalactamase is a very efficient enzyme.
                                                                                                                                                                                                                                                                                                                                               12-FEB-1998 (first entry)
Mutagenic PCR primer 7 for the TEM-1 betalactamase gene.

TEM-1 betalactamase gene; gene reassembly reaction; DNA library;
gene shuffling; random fragmentation; mutagenesis; recombination;
GFP protein; arsenate detoxification bacteria; cefotaxime;
cadmium detoxification bacteria; drug resistance gene; PCR primer
                                                                                                                              Generating polynucleotide(s) with desired characteristics by iterative selection and recombination - used for the directed molecular evolution in vitro or in vivo of proteins, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V54906 standard; DNA; 42
V54906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ttctcagaa 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 100.0%;
Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
CO introduce E104K mutation into TEM-1 betalactamase gene.
CHAMBASE gene; recombination; gene shuffling; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9;
Pred. No.
0; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 49; I
1.37e+03;
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                                                                                                                                                                                                                                                                                                                                                    gene; PCR primer;
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CC obetalactamase genes were used in a novel method to construct mutant
CC combinations of the gene, which produce enzymes with a greater activity.
CC The method involves recombining at least 2 forms of the polynucleotide to
CC produce a library of recombinant forms of the sequence. The library is
CC screened for a recombinant sequence, which is then recombined with
CC another form of the polynucleotide, the same or different from the first
CC another form of the polynucleotide, the same or different from the first
CC polynucleotides. The subsequent libraries are screened, and recombination
CC performed until the recombinant polynucleotide has acquired the desired
CC property. The methods are used to reassemble DNA after random
CC in vivo recombination. The repeated cycles of mutagenesis, shuffling and
CC in vivo recombination. The repeated cycles of mutagenesis, shuffling and
CC of proteins. In particular the methods are used for the production of
CC mutant CFP protein which has been modified to show enhanced fluorescence
CC when used as a reporter of gene expression and regulation. Also
CC cadmium detoxification bacteria, drug resistance genes and variant
CC consumerases.
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                                                                                                                                                                                                                Nucleic acid multimer for hybridisation assays
having single-stranded oligo-nucleotide units
capable of binding specifically to sequences of interest.
Fig. 10-2; 112pp; English.
Partial nucleotide sequences of the capture and amplifier
the TEM-1NH assay. The capture probe is complementary to t
strand of N. gonorrhoeae Tem-1 beta lactamase gene. It is
temkit21.18.
Sequence 50 BP; 11 A; 11 C; 15 G; 13 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementary strand of the Neisseria gonorrhoeae Tem-1 beta lactamase gene combined with 11a2c amplifier probe Neisseria gonorrhoeae; beta lactamase Tem-1; capture probe; amplifier probe 11a2c; temkit21.18; TEM-1NH assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Urdea MS, Warner B, Running JA, Kolberg JA, Clyne
WPI; 89-150787/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 33
N91955 standard; DNA; 50 BP.
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14-OCT-1988; U03644.
30-SEP-1988; US-252638, US-109282.
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                               ttctgagaa 13
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                                                                                                                                        Similarity
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larity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /"capture probe"
31..50
/*tag= b
/"lla2c amplifier probe"
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Pred. 1
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. No. 1.37e+03;
Mismatches 0;
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                                                                                                                                        1.37e+03
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the coding
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The present invention describes enzymatic nucleic acid molecules (NAMs)

Chaim 7; Page 90; 109pp; English.

Chaim 8; Page 1; Page 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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cross-linked enzyme donor polypeptide - which has reduced complementation activity with enzyme acceptor polypeptide and may be used in assays for e.g. viral protease

Example 5; Page 20; 36pp; English.
This sequence represents an amplification primer for a beta-galactosidase alpha region (ED7) linked to a 8 residue (p17/p24) HIV protease recognition site. The amplified sequence encodes a polypeptide of the invention. The polypeptide of the invention is a cross-linked enzyme donor polypeptide having an amino acid sequence substantially identical to the N-terminal or C-terminal of native beta-galactosidase is. The . . . amino acid sequence has 2 cysteine residues intramolecularly linked via a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC.
(UYAS-) UNIV ASTON.
Akhtar S, Fell P, McSwiggen JA;
WPI; 98-437449/37.
Enzymatic nucleic acids - which cleave RNA derived growth factor receptor, useful for inhibiting cell
                                                                                                                                                                                                                                                                                       31-JUL-1997. 001129.
23-JAN-1997; U01129.
26-JAN-1996; US-592013.
(BOEF ) BOEHRINGER MANNHEIM CORP.
Elsenbels SJ, Khanna P, Lingenfelter Powell MJ, Tietze LF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     viral protease detection, or.
Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1998 (first entry)
N-terminal primer for ED7-HIV p17/p24 gene.
PCR primer; amplify; beta-galactosidase alpha region; ED7;
HIV protease recognition site; cross-linked enzyme donor p
viral protease detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T99091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1998. U00730.
14-JAN-1998; U00730.
04-DEC-1997; US-985162.
31-JAN-1997; US-936476.
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Synthetic
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17-мак-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 54 BP
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llarity 66.7%;
Conservative
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1.37e+03;
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EGF-R;
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cell proliferation;
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                                       04-MAY-1994.
19-AUG-1993; 113261.
28-AUG-1992; US-938084.
(HOFF) HOFFMANN LA ROCHE &
(HOFF) HOFFMANN LA ROCHE &
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02-DEC-1997; U21748.
03-DEC-1996; US-758306.
(RIBO-) RIBOZYME PHARM INC.
MCSwiggen JA, Stinchcomb DT;
MPI; 98-333332/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer, autoimmune disease and allergies Claim 11; Page 39; 61pp; English. The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA. V93889 to V94574 represent specifically claimed ribozymes, and V94575 to V95260 represent specifically claimed substrate sequences from the present invention. The ribozymes can be used for the treatment of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy and other inflammatory conditions. The ribozymes are also used to induce tolerance in a recipient to alloantigen from a donor. sequence 54 BP; 17 A; 11 C; 11 G; 15 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disulphide bond, or has 2 reactive amino acid residues intramolecularly linked via covalent attachment of the residues to a cross-linking agent, such that complementation of the enzyme donor polypeptide with an enzyme acceptor polypeptide is inhibited. The enzyme donor polypeptides may be used in assays, e.g. for viral proteases (see w09727320). Such assays can be carried out with extremely low inherent background signal. Sequence 54 BP: 14 A; 14 C; 10 G; 16 T;
                                                                                                                                                                                                                                                                                 Oligonucleotide probe for repeated sequence of D1721 locus. Probe; detection; repeat sequence; D1721; locus; control region; conserved sequence; human alpha satellite locus; mitochondria; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IL-2 receptor g-chain hairpin ribozyme position 1419.
Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
autolmmune disease; psoriasis; allergy; inflammatory disease;
                                                                                                                                                                                                                             EP-594959-A.
                                                                                                                                                                                                                                                              Synthetic.
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V94164 standard; RNA; 54 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q62540 standard; DNA; 60 BP
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W09824913-A2.
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Local Similarity 100.0%;
nes 9; Conservative
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DR PPSDB; R29523.

PT plasmid pAP-1 and expression vectors for transforming bacterial pT cell - contains recombinant DNA for encoding coupled Escherichia pT cell - contains recombinant DNA for encoding coupled Escherichia pT coll surface antibody and PAL pS Example 1; Fig lb; 6pp; German.

CC The PAL gene from E.coli was amplified in plasmid pRC2 using the CC polymerase chain reaction. The upstream primer introduces a BanHI CC site at the 5'end of the gene resulting in the substitution of CYs at position 1 of PAL by Gly. The amplified PAL sequence was ligated CC to DNA fragments coding for the variable regions of heavy and light CC chains of a humanised chicken lysozyme antibody joined via a DNA CC fragment encoding an 18-amino acid sequence representing the epitope CC YOL/34 (the "TAG-linker"). Immediately upstream of the VH gene were CC ligated a promoter/operator region, RBS and pelB leader sequence. The CC resulting plasmid was designated pAP-1 and can be used for the rapid cC screening of antibody gene banks, e.g. to isolate antibody against thumour-associated antigen. See also Q25907-8 and Q26743-6.
                                                                                                                                                                                                                                         RESULT OF STATE OF ST
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30-JUL-1992.
08-JUL-1991; 122598.
R 08-JUL-1991; DE-122598.
QDEKR-) DEUT KREBSFORSCHUNGSZENT STIFTUNG.
Preitling F, Duebel S, Fuchs P, Little M;
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This oligonucleotide probe is complementary to a region in the 2.7 kilobase D1721 locus, a highly repetitive sequence. The use of probes complementary to a highly repeated sequence or to a conserved sequence provides high detection sensitivity and specificity. The probe may be optionally labelled with biotin and used in methods to quantitate the amount of DNA in a sample. See Q62532-51.
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Epitope YOL1/34 coding sequence in pAP-1.
Peptidoglycan-associated lipoprotein; polymerase chain reaction;
tumour-associated antigen; antibody gene bank; screening;
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i.e. the YOLI/34 epitope"
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                                                                                                                   Pred.
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. 1.37e+03;
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N60749 standa N60749; N60749; O8-JUN-1991

standard; DNA; 77 BP

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Matches
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D 3-JUN-1997.

F 11-JUN-1990. 536428.

R 11-JUN-1991. US-536428.

R 11-JUN-1991. US-536428.

R 11-JUN-1991. US-531473.

R 11-JUN-1992. US-931473.

R 21-OCT-1992. US-946624.

R 19-MAY 1995. US-447172.

R 19-MAY 1995. US-447172.

R 07-JUN-1995. US-447173.

R 19-MAY 1995. US-447330.

A Allen P, Gold L:

R Nucleic acids that are HIV-1 nucleocapsid ligands of HIV-1 infection

T Nucleic acids that are HIV-1 nucleocapsid ligands - fc

T Nucleic acids that are HIV-1 nucleocapsid of diagnosis or HIV-1; 17pe 11gands of TP9101-T79122 are RNA ligands for the nucleocapsid of immunodeficiency virus type 1 (HIV-1). The ligands bin nucleocapsid and inhibit its function, they can be use treatment and diagnosis of HIV-1 infection.

Q Sequence 77 BP; 18 A; 22 C; 20 G; 17 U;
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16-DEC-1985;
26-DEC-1984;
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The analgesic endocrine hormone endorphin was prepd. by synthesis the individual oligonucleotide blocks; linking of the individual blocks by solid-phase synthesis on aminated CPG to give the gene; synthesis of the double-stranded DNA and combination of it with a vector plasmid; cloning of the resulting gene-contg. plasmid; and culture of the transformed E. coli JM-103 strain produced. CPG is
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US5635615-A.
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C-1984; JP-281645.
) NIPPON SHINYAKU
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gand to HIV-1 nucleocapsid.
immunodeficiency virus; HIV; nucleocapsid;
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Similarity 100.0%;
9; Conservative
                                                                                         Similarity 66.7% 6; Conservative
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controlled pore glass; solid-phase
Location/Qualifiers
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77 BP; 17
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Pred. No.
0; Misma
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1.37e+03;
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CA single-stranded DNA (or its complementary strand or the corresp. CC double-stranded DNA) which comprises one of the 7837 "GS" sequences cc given in T19001-T26837 and which is able to hybridise to part of CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) cs sequences were obtained from 3'-directed cDNA libraries prepared cC from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-c untranslated sequence is unique to a particular mRNA species, almost call the 3'-oriented cDNAs hybridise with specific mRNAs. Each library call the 3'-oriented so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be cerognising different cell types.

So sequences as means of diagnosing abnormal cell function or for recognising different cell types.

So sequence 79 BP; 18 A; 19 C; 12 G; 30 T;
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Best Local S
Matches
                                                                                      16-DEC-1985; 544459.
26-DEC-1984; JP-281645.
(NOSH) NIPPON SHINYAKU K
Yano J;
WPI; 86-177271/28.
P-PSDB; P60832.
                                                                                                                                               DE3544459-A.
03-JUL-1986.
16-DEC-1985;
26-DEC-1984;
                                                                                                                                                                                                                          Hormone;
Key
cds
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Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
Long-chain DNA e.g. endorphin gene prodn. - by solid-phase coupling of oligo:nucleotide blocks on aminated controlled pore glass CPG as carrier by triester method Example; page 8; 18pp; German.

The analgesic endocrine hormone endorphin was prepd. by synthesis the individual oligonucleotide blocks; linking of the individual
                                                                                                                                                                                                                                                                                                   N6075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                    Sequence
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WPI; 95-206931/27.
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N60751 standard;
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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(OKUB/) OKUBO K.
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controlled pore glass; soll
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larity 100.0%;
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27-ApR-1993; US-876285.

2 29-ApR-1993; US-876285.

R 21-JU1-1993; US-918313.

R 15-JAN-1993; US-918313.

A (HOSP-) HOSPITAL FOR SICK CHILDREN.

A (UNNE:) UNITED MEDICAL & DENTAL SCHOOL GUYS.

PI Buchwald M, Mathew CG, Strathdee CA, Wevrick R;

PI Buchwald M, Mathew CG, Strathdee CA, Wevrick R;

PI Human cDNA which complements Fanconi Anaemia gp. C

PT Human cDNA which complements fanconi Anaemia gp. C
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EP-594959-A.
04-MAY-1994
19-AUG-1993; 113261.
28-AUG-1992; US-938084.
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Claim 1: Page 111: 137pp; English.

The sequences given in Q5129-54 represent the 5' and 3' splice regions of the introns from the Fanconi Anemia Group C Complementing (FACC) DNA. Three cDNA molecules which are cellular varients of a single cDNA, are transcribed from the FACC gene. The three cDNAs each contain an identical open reading frame encoding the FACC protein may be used for the diagnosis and study of fanconi anemia. The FACC gene and cDNAs may be used in gene therapy. Sequence 80 BP; 19 A; 15 C; 14 G; 31 T;
Reynolds RL, Walsh PS;
WPI; 94-145673/18.
Oligo:nucleotide probes
sequences complementary
                                                                                                                                                                                                                                                                                                                                                  06-DEC-1994 (first entry)
Oligonucleotide probe for repeated sequence of D1721 locus.
Probe; detection; repeat sequence; D1721; locus; control reconserved sequence; human alpha satellite locus; mitochondr
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Claim 1
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Sequence 80 BP; 15 A; 20 C; 22 G; 23 T;
                                                                                                              (HOFF ) HOFFMANN LA
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Q62542 standard;
Q62542;
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W09322435-A.
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           for detecting human DNA - having to a human alpha satellite locus
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mitochondria; ss.
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                                                                                                        Homo sapiens.

W09521938-A1.

17-AUG-1995.

14-FEB-1995; E00553.

14-FEB-1994; EP-200377.

(UTLE') RIJKSUNIV LEIDEN.

Bertina RM, Reitsma PH;

WPI; 95-293134/38.
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This oligonuclectide probe is complementary to a region in the 2.7 kilobase D1721 locus, a highly repetitive sequence. The use of probes complementary to a highly repeated sequence or to a conserved sequence provides high detection sensitivity and specificity. The probe may be optionally labelled with biotin and used in methods to quantitate the amount of DNA in a sample. See Q62532-51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligo:nucleotide probes for detecting human DNA - having sequences complementary to a human alpha satellite locus or a conserved sequence in the mitochondrial genome Claim 6; Page 15; 27pp; English.

This oligonucleotide probe is complementary to a region in the 2.7 kilobase DI721 locus, a highly repetitive sequence. The use of probes complementary to a highly repeated sequence or to a conserved sequence provides high detection sensitivity and specificity. The probe may be optionally labelled with biotin and used in methods to quantitate the amount of DNA in a sample. See Q62532-51. Sequence 130 BP; 32 A; 26 C; 28 G; 44 T;
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Q62537
Q62537
Screening for genetic defect associated with thrombosis anticoagulant response to activated protein C - useful homozygosity or heterozygosity for a mutation in Factor
                                                                                                                                                                                                                                                                                                                                                                                                                   20-DEC-1995 (first entry)
Human Factor-V intron 10.
Factor-V; thrombosis; thrombosis; anticoagulant; activated protein-C; APC; homozygosity; heterozygosity; ss.
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T03931 standard;
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19-AUG-1993; 113261.
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1.37e+03;
2ag 0;
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. 1.37e+03;
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   to determine v, va, VIII
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PF 12-FEB-1992; US-837195.

PR (USSH) US DEPT HEALTH & HUMAN SERVICE.

PR (USSH) US DEPT HEALTH & HUMAN SERVICE.

PI Adams MD, Moreno RF, Venter CJ;

PI Rathers for human genes transcribed in-vivo, facilitate tagging pr markers for human genes transcribed in-vivo, facilitate tagging pr of most human genes transcribed in-vivo, facilitate tagging pr of most human genes transcribed in-vivo, the can be used as markers CC library as part of a large set of ESTs which can be used as markers CC for human genes transcribed in vivo. They can be used to facilitate CC tagging of most human genes, for mapping locations of expressed genes con chromosomes, for individual or forensic identification, for mapping CC locations of disease-associated genes, for dentification of tissue CC type, and for prepn. of antisense sequences, probes and constructs. CC EST01247 has a "poor" coding probability as evaluated using the CC coding-region prediction program CRM. See also Q59041-Q61440.
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04-NOV-1992.
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Disclosure; Page 70-71;
Human Factor-V intron 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-1994 (first entry)

Human brain Expressed Sequence Tag EST01247.

Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; s
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                                                                                                                                                                                    PCR product prepared using primer WBS2. PCR; chromosome specific repeated DNA; cytogenetics; interphase nuclei; metaphasomatic cells; ss.
                                                                                                                                                                                                                                                                                                                             T 48
Q30026 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genotyping, to detect the 1691A allele resistance.
                        (REGC
                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                   Q30026;
18-MAR-1993
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Q61212;
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1992; 303159.
1-1991; US-683441.
1-1992; US-858124.
) UNIV CALIFORNIA.
W, Weier HUG;
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larity 100.0%;
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1.37e+03;
1.37e 0; Indels
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Claim 16; Page 18; 25pp; English.
Claim 16; Page 18; 25pp; English.
This sequence represents that of the insert of plasmid pBS609-51
created by the ligation of the PCR product prepared using primer
WBS2 (Q30017) into pBS. PCR primer Q30017 is used to amplify a
region of the 171 bp alpha satellite (alphoid) repeat sequence,
conserved in all human chromosomes. This binds to the alpha
satellite repeat concensus sequence. The minimal product size
expected is 175bp, and is used as a probe for the repeat sequenc
of human centromeres.
61 A; 37 C; 43 G; 56 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-1992.

09-APR-1992; 303159.

09-APR-1993; US-683441.

26-MAR-1992; US-858124.

(REGC ) UNIV CALIFORNIA.
                                                                                      T79775 stand
T79775;
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10-NOV-1997
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Q30027;
18-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 18; 25pp; English.

This sequence represents that of the insert of plasmid pBS609-52 created by the ligation of the PCR product prepared using primer WBS4 (Q30018) into pBS. PCR primer Q30018 is used to amplify a region of the 171 bp alpha satellite (alphoid) repeat sequence, conserved in all human chromosomes. This binds to the alpha satellite repeat concensus sequence. The minimal product size expected is 175bp, and is used as a probe for the repeat sequence of human centromeres.

Sequence 197 BP; 60 A; 35 C; 42 G; 60 T;
Potato starch branching enzyme gene intron starch branching enzyme; SBE; potato; gene transgenic plant; starch production; modifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR product prepared using primer WBS4.

PCR; chromosome specific repeated DNA; chromosome staining;

cytogenetics;interphase nuclei; metaphase spreads; germ line cells;
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nucleotide primers - useful for chromosome
for staining agent in cyto genetic analysis
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WPI; 92-367577/45.
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Deoxyribonucleic acid amplification using degenerate oligo Deoxyribonucleic states - useful for chromosome specific repeated DNA for staining agent in cyto genetic analysis by polymerase chain
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Pred. No.
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  intron 6.
; genetic engineering;
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1.37e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA (or its complementary strand or the corresp. Could ouble-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA ilbraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 209 BP; 51 A; 31 C; 40 G; 86 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-1996; E03053
14-JUL-1995; GB-014
(DANI-) DANISCO AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Affecting enzymatic activity in plant by expressing sense intron sequence - esp. for inhibiting starch branching enzyme to create modified starch without post-harvest derivatisation

Claim 8: Page 31: 70pp: English.

T79775 represents intron 6 of the potato starch-branching enzyme
(SBE) gene. Sequences antisense to introns of the SBE gene are used to produce transgenic plants producing modified or new forms of starch for industrial use. The sequences allow starches to be made without post-harvest modification (which uses hazardous chemicals and requires much energy). Using the antisense intron sequences is more reliable, efficient and selective than known methods for regulating enzymatic activity because there is almost no homology between introns in different SBE genes. The SBE gene promoter (see T79783) is also
                                                                                                                                                                                                                                                                                                                                                                                                                                   (MATS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; decell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                       Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                             Matsubara K, Okubo K;
WPI; 95-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T22515 standard; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 97-132651/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuber W09704113-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human gene signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%;
Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
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1.37e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 198
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Query Match

100.0%;

Score

9.

DB

20;

Length 209;

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TRESULT
ACCOMENTATION
ACCOMENT
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Best Local 9
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Matches 9; Conservative
            Matches
                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                   04-OCT-1994.
08-OCT-1992; JP-309167.
08-OCT-1992; JP-309167.
(NORI-) NORIN SUISANSHO NOGYO SEIE
(TAKE) TAKEDA CHEM IND LTD.
WPI; 94-353746/44.
Identification of plants at the DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preserve known preservence 218
                                                                                                                          sequences as probes

Claim 6; Page 10; 41pp; Japanese.

Claim 6; Page 10; 41pp; Japanese.

The nucleotide sequence of the retrotransposon probe Tos12 cloned from the rice plant Oryza sativa. The probes may be used for the analysis plant genes to secure the efficient identification of plants and genet uniformity for the production of pure lines, inbred parent lines and near-isogenic lines.

Sequence 243 BP; 67 A; 33 C; 57 G; 86 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the placenta or bone marrow comprise any of: (A) a seque selected from (076401-077613), (B) an allelic variation sequence as described in (A), or (C) a sequence common to (A) or (B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JAN-1994.
13-JUL-1993; G01467.
13-JUL-1992; GB-014857.
(MEDI-) MEDICAL RES COUNCIL.
Gross J. Hadfield KM, Howe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retrotransposon;
pure line; inbre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid fragment encoding for genetic analysis and mapping Claim 1; Page 560; 616pp; English. Human nucleic acid fragments, isola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brain; placenta; bone marrow; genetic analysis; gene mapping; detection; homology; human; adrenal tissue; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brain; placer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 52
Q77502 standard; DNA; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-1995 (first e
Retrotansposon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 94-035056/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sibson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preferred sequences
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 standard; DNA; 243 BP.
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                                     h 100.0%;
Similarity 100.0%;
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R, Starkey M;
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            Conservative
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BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                robe Tos12, cloned from Oryza sativa.
probe; rice; plant; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parent line; near-isogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              se.
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Score 9;
Pred. No.
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Pred. No.
0; Misma
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0; M
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               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (C) a sequence complementary
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                                                                                                                                                                                                                                                                                                                                                                      level - using retrotransposon
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1.37e+03;
                                        DB 13; L
1.37e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 G;
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                                                                     Length 243;
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               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pr New polynucleotides encoding human secreted proteins - derived from Pr e.g. human blood, kidney, foetal lung, placenta, testes, brain, pr e.g. human blood, kidney, foetal lung, placenta, testes, brain, pr ovary, pituitary, retina and colon cDNA libraries
Pr ovary, pituitary, resquence isolated from a variety of human tissue color are all secreted EST sequences isolated from a variety of human tissue cources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and color treating, preventing or ameliorating defical conditions in humans and color animals, although no supporting data is given. Suggested activities
Province activity, chemotactic/chemokinetic activity, haemostatic activity, catherin/tumour invasion suppressor activity, tumour inhibition activity, receptor/ligand activity, tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local s
Matches
                                                                                                                                                                                                                                                                     793999;
24-FEB-1998 (first entry)
24-FEB-1998 (first entry)
Model pre-therapeutic RNA molecule.
Diphtheria toxin; subunit A; human chorionic gonadotropin; HCG;
Diphtheria toxin; subunit a; human chorionic gonadotropin; HCG;
prostatic hypertrophy; pre-therapeutic molecule; Gaucher's disease;
prostatic hypertrophy; pre-therapeutic molecule; Gaucher's disease;
functional therapeutic RNA; splicing; human immunodeficiency virus;
functional therapeutic RNA; splicing; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST clone HR693.

Expressed sequence tag; secreted protein; haematopolesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                misc_feature
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EST clone H
                              misc_feature
                                                                                                                                                                                                                                      misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1998; U06956.
10-APR-1997; US-837312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEMY ) GENETICS INST INC
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Similarity 100.0%
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST sequences are also stated
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                           23..53
/*tag=
/note=
60
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/*tag=
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                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 A;
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                                                         "spacer region"
                                                                                                                                              "complementary to the target sequence of adenovirus 2 major late promoter"
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to be useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 251;
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PE Example 2; Page 18; 47pp; English.

CC The present sequence represents a model pre-therapeutic RNA molecule comprising a binding region for target pre-mRNA, at least one of 3' and CC 5' splice sites, sequences functional as RNA or sequences encoding a CC therapeutic or useful protein or gene product (e.g. subunit A of CC elements required for splicing and production of a therapeutic RNA. CC elements required for splicing and production of a therapeutic RNA. CC elements required for splicing and production of a therapeutic RNA. CC elements required for splicing and production of a therapeutic RNA. CC elements required for splicing and production of a therapeutic RNA. CC elements required for splicing and the HSV protein marker allows for detection using monoclonal antibodies. Pre-therapeutic molecules are CC detection using monoclonal antibodies. Pre-therapeutic molecules are used to produce functional therapeutic RNA or nucleic acid analogues in Specific target cells, which may be present in animals, plants, and CC especially humans. The pre-therapeutic molecule does not have to be targeted to a particular type of cell, as the the therapeutic molecule CC targeted to a particular type of cell, as the the therapeutic molecule CC targeted with virus (e.g. human immunodeficiency virus) or other CC pathogens, benign and malignant neoplastic cells (e.g. prostatic constance of the immune system involved in autoimmune constance of the product generates and tissue rejection. Otherwise the product generates and tissue rejection. There are now gene product of the promable expressed
                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                T01037 stands
T01037;
07-MAY-1996
                               counter receptor; transgenic
Mus musculus.

Location/Qual
cds
1.:138
 WO9523859-A2
                                                                                                 T-cell costimulatory molecule;
                                                                                                              Mouse B7-2
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                therapeutic protein, marker or new gene product not normally expressed in these cells, e.g. for treatment of inherited diseases (e.g. Gaucher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New pre-therapeutic RNA converted to active form by only in cells containing specific pre-mRNA, used to toxins for targeted killing of cells such as tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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                                                                                                                                                                                                                                               38 ttctgagaa
                                                                                                                                                                                                                                 25 ttctgagaa
                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                             100.0%;
Similarity 100.0%;
9; Conservation
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                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                 258 BP; 68 A;
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128..145
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/note=
84..85
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61..83
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/note= "histidine protein marker"
151..153
                                                Location/Qualifiers
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                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                 a missing/defective gene.; 72 C; 64 G; 54 T;
                                                                                                                                                                                                                                                                                               Score 9;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splice
                                                                               .e; B7-2;
: animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein marker'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site'
                                                                                                 T-lymphocyte;
                                                                                 immunoglobulin;
                                                                                                                                                                                                                                                                                                                  DB 35; Le
1.37e+03;
                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                  Length 258;
                                                                                                 CD28; CTLA4;
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o generate, e.g.
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                                                                                                                                                                                                                                                                                                                                                                PI Albertini RJ, Falta MT;

PI Albertini RJ, Falta MT;

Preventini RJ, Falta MT;

Preventing or reducing severity of diabetes - by inhibiting the preventing or reducing severity. By interfering with activity of specific T-cells, partic. by interfering with processor activity of specific T-cell receptors

PI diabetes-associated T cell receptors

CC DNA sequences (096132-34) coding for non-conserved regions of T-cell cell receptor (TCR) beta-14 (R78688-88) may be operatively linked to expression CC control sequences and incorporated into vectors. These vectors are directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of a diabetic care directly injected into e.g. the skeletal muscle of T cell care directly injected into e.g. t
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Best Local Similarity 100.0%;
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02-MAR-1995; U02576.
02-MAR-1994; US-205697.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
(DAND ) DANA FARBER CANCER INST.
BOTTIGHLO F, Freeman GJ, Nadler LM
WPI; 95-320574/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09521623-A1.
17-AUG-1995
10-FEB-1995; U01572.
14-FEB-1994; US-192963.
(UYVE-) UNIV VERMONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 80; 11pp; English.

Exon 5 (T01037) of the mouse T-cell costimulatory molecule B7-2
gene encodes the cytoplasmic domain (R82890) of B7-2. It can
be used to construct nucleic acids coding for novel cytoplasmic
forms of T-cell costimulatory molecules that also incorporate a
second cytoplasmic domain. Such T-cell costimulatory molecules bind
to CD28 or CTLA4 and trigger a costimulatory signal in T-cells.
Sequence 261 BP; 97 A; 52 C; 59 G; 53 T;
                                                V69007; standard; V69007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel T cell co-stimulatory molecules - occurring alternatively spliced forms of molecules or variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-1996 (first entry)
T-cell receptor beta-chain variable region V-beta-14-encoding DNA.
Diabetes; adoptive immunotherapy; gene therapy;
22-JAN-1999 (first entry)
DNA molecule encoding a polypeptide for detecting breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell receptor beta-chain; ss.
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Q96134 standard; DNA; 282 BP
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                                                                                                                                                                            33 ttctcagaa 25
                                                                                                                                                                                                      69 ttctcagaa 77
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                                                                                                                                                                                                                                                                              Conservative
                                                                             DNA;
                                                                             293
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Pred. No. 1.37e+03
0; Mismatches (
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Pred.
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to naturally T cells co-stimulatory
                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                       Length 282
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PAR (CORT.) CORTAX CORP.
PI Frudakis TN, Reed SG, Smith JM;
PI RMP; 98-557473/47.

PT New DNA sequences isolated from endogenous human retroviral element
PT and related vectors, transformed cells, proteins and antibodies,
PT useful for diagnosis, treatment and prevention of breast cancer
PS Claim 11; Page 65; 173pp; English.
CC wiseful for diagnosis, treatment and prevention or measurement of
CC useful in detecting human breast cancer. Detection or measurement of
CC useful in vaccines for inhibiting development (for grevention or
CC useful in vaccines for inhibiting development (for prevention or
CC therapy) of breast cancer. The polypeptides may also be used to
CC raise monoclonal antibodies, used as immunoassay reagents.
SQ Sequence 293 BP; 66 A; 43 C; 48 G; 73 T;
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PD 15-027-1998; U06956.

PR 10-APR-1997; US-837312.

PR 10-APR-1997; US-837312.

PR 10-APR-1997; US-837312.

PR (GEMY) GENETICS INST INC.

PA (GEMY) GENETICS INST INC.

PA (GEMY) GENETICS INST INC.

PA Agostino MJ; Jacobs K, Lavailie ER, McCoy JM, Merberg D,

PR Racie LA, Spaulding V, Treacy M;

PI Racie LA, Spaulding V, Merberg D,

PI Racie LA, Spaulding V, Merberg D,

PI Racie LA, Spaulding P,

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Best Local Similarity
Matches 8; Consei
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Expressed sequence tag; secreted protein; haematopolesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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V87805;
12-FEB-1999 (first entry)
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11-DEC-1997; US-991789.
09-APR-1997; US-838762.
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W09845437-A2.
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e; epitope; endogenous; retroviral element; ss.
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                                              The EST sequences are
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Matches
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N50452; standard; RNA; 297 B
12-MAR-1992 (first entry)
Hop stunt viroid RNA.
HSV; ss.
                                                                                                                                                                                                                                 US5736318-A.
07-APR-1998.
17-MAR-1995: US-406248.
17-MAR-1995: US-406248.
(HARD ) HARVARD COLLEGE.
(HARD ) UNIV HARVARD.
Jones DL, Munger K;
WPI: 98-239202/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V16717 standard; DNA;
V16717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure: Fig 1; 14pp; Japanese. The RNA folds back on itself to fo corresponding to the RNA can be in these used for the introduction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1985.
17-AUG-1983;
17-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New plasmid(s) with consecutive fractions contg. cDNA to plant virus RNA, for introducing exogenous genes into cells etc.
Evaluation of proliferative state of cells transformed with human papilloma virus - by determining cyclin-dependent kinase activity induced by E7 onco-protein Disclosure; Columns 19-20; 14pp; English.

The present sequence encodes Human papillomavirus (HPV), strain 16, E7 oncoprotein. The proliferative state of a cell transformed with HPV can be evaluated in the following manner. Cyclin-dependent kinase complexes containing protein P21CIPI (W46887-88) are isolated from the transformed cell, and the HPV E7 oncoprotein added to the isolated protein. Cyclin-cyclin-dependent kinase complexes are isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E7 oncoprotein; proliferative state; HPV; kinase active cyclin/cyclin-dependent kinase; p2lCIP1; interaction; cyclin/cyclin-dependent kinase inhibitor; ss.
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J60041486-A.
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E7 oncoprotein; proliferative
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JP-149815.
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1.37e+03;
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V; kinase activity;
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Matches
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R P-PSDB; R46087.

I cDNA of human origin and proteins coded by it - which may expressed by in vivo or in vitro translation using sense for antisense DNA corresponding to the cDNA.

S Claim 1; Page 41-42; 167pp; Japanese.

S Claim 1; Page 41-42; 167pp; Japanese.

MRNA expressed in human fibrosarcoma cell line HT-1080 was isolated and used to construct a cDNA library using vector pKAL. Clone HP00062 encoding Zn resistant-like protein was isolated.
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04-AUG-1993; J01095.
04-AUG-1992; JP-208077.
13-NOV-1992; JP-327619.
26-FEB-1993; JP-061431.
(SAGA ) SAGAMI CHEM RES CENTRE.
IWADOTI A, KATO S, KATO T, KIM N.
WPI; 94-065588/08.
                                 20-JAN-1994.

13-JUL-1993; GB-01467.

13-JUL-1992; GB-014857.

(MEDI-) MEDICAL RES COUNCIL.

Gross J, Hadfield KM, Howell

Sibson DR, Starkey M;

WPI; 94-035056/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from an untransformed cell that is substantially homogenic with the transformed cell, and the HPV E7 oncoprotein added. The kinase action of the 2 samples are measured, where a proliferating transformed cell has a greater kinase activity that the untransformed cell. The meth used for determining the extent of interaction and/or inactivation between a cyclin/cyclin-dependent kinase inhibitor and the HPV E7 oncoprotein and thus evaluating the proliferative state of a transf
                                                                                                                                                                                                                                                                                                                    Q76420
Q76420;
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Q57426;
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                                                                                                                                                                                                                                Human genome fragment. (Preferred)
Brain; placenta; bone marrow; genetic analysis;
detection; homology; human; adrenal tissue; ds.
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V87753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of most human genes

Example 4; page 374; 500pp; English.

Example 4; page 374; 500pp; English.

The Expressed Sequence Tag was isolated from a human brain cDNA
library as part of a large set of ESTs which can be used as markers
for human genes transcribed in vivo. They can be used to facilitate
tagging of most human genes, for mapping locations of expressed genes
on chromosomes, for individual or forensic identification, for mapping
locations of disease-associated genes, for identification of tissue
type, and for prepn. of antisense sequences, probes and constructs.
EST90813 has a "poor" coding probability as evaluated using the
coding-region prediction program CRM. See also Q59041-Q61440.

Sequence 325 BP; 100 A; 35 C; 60 G; 127 T;
                                                                                                                                               EST clone EQ187.

Expressed sequence tag: secreted protein; haematopolesis regulator tissue growth; activin; inhibin; tumour invasion suppressor; EST; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           markers
of most
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Human nucleic acid fragments, isolated from brain adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (Q76401-Q77613), (B) an allelic variation of a sequence as described in (A), or (C) a sequence complementary
                       15-OCT-1998.
10-APR-1998; U06956.
10-APR-1997; US-837312.
                                                                                                     Homo sapiens.
W09845437-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain Expressed Sequence Tag EST00813.
Gene transcription product; genetic markers; tagging; in vivo;
transcription; mapping; locations; chromosomes; chromosomal; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence known per se. Sequence 314 BP;
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Preferred sequences exhibit no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1993; U01294.
12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH
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Claim 1, Page 167-168; 641pp; English.

CC The present sequence represents an expressed sequence tag (EST), and is

CC a polynucleotide of the invention. The polynucleotides of the invention

CC are all secreted EST sequences isolated from a variety of human tissue

CC sources. The EST sequences and proteins encoded by them are predicted to

CC have useful biological activities which would make them suitable for

CC treating, preventing or ameliorating medical conditions in humans and

CC animals, although no supporting data is given. Suggested activity,

CC haematopolesis regulating activity, tissue growth activity, haemostatic

CC activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, chemotactio/themokinetic activity, anti-inflammatory

CC activity. The EST sequences are also stated to be useful for gene
                                                                             Claim 1; Page 985-986; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. Codouble-stranded DNA) which comprises one of the 7837 "GS" sequences given in 719001-726837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 329 BP; 124 A; 43 C; 59 G; 101 T;
Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying gene signatures in for diagnosis of abnormal cell reflects relative abundance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsubara K, Okub
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T21863 standard; cDNA to mRNA; 329 T21863;
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Racie LA, Spaulding
WPI; 99-070078/06
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33 ttctcagaa
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Similarity 100.0%;
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Example 1; Page 122; 500pp; English.
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from the used as markers
for human genes transcribed in vivo. They can be used to facilitate
tagging of most human genes, for mapping locations of expressed genes
on chromosomes, for individual or forensic identification, for mapping
locations of disease-associated genes, for identification of tissue
type, and for prepn. of antisense sequences, probes and constructs.
EST00070 has a "poor" coding probability as evaluated using the
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12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
Adams MD, Moreno RF, Venter CJ;
WPI; 93-272882/34.
Enriched oligonucleotides and corresp. sequences - used a corresp. sequences - used a corresp.
Claim 1; Page 2027; 2245pp; Japanese. A single-stranded DNA (or its complementary double-stranded DNA) which comprises one of given in T19001-T26837 and which is able to human genomic DNA, cDNA or mRNA is claimed.
                                                                                                                                                            tissues
Claim 1
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Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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Q59108;
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WPI; 95-206931/27.
Identifying gene signatures in
for diagnosis of abnormal cell
reflects relative abundance of
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12-NOV-1993;
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the 7837 "GS" sequences
hybridise to part of
The GS (Gene Signature)
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                                                                                                                                                                                              PS Disclosure; Page 56; 95pp; English.

CITH'S sequence is part of the human chromosome 21 centromere, and can be cused in the DNA construct of the invention. The construct is a mammalian cartificial chromosome (MAC), and comprises a mammalian telomere and a centromere, where the centromere has a DNA sequence containing copies of the CENP-B box sequence. The invention also relates to methods for cetablishing yeast artificial chromosomes (YACs) comprising mammalian ctelomeres and centromeres. The method can be used to construct, modify and stably maintain YACs in yeast cells which have the ability to form CC dateonomously, be stably maintain cells. The MACs can replicate cautonomously, be stably maintained extrachromosomes and transmitted confictently in mammalian cells. The MACs can be used for basic studies on coganisation and function of mammalian chromosomes and also as a vector to introduce DNA segments (genes) of interest to test their functions in the subject to variable expression due to integration position effect nor cause unpredictable insertion mutation on host chromosomes. Furthermore CC MACs will have the capacity to accommodate a DNA segment up to megabases where an entire large gene or group of genes and regulatory elements could be included. The MACs can be used for somatic gene therapy or to
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26-AUG-1996; WO-J02381.
(KENO/) IKENO M.
(MASU/) MASUMOTO H.
(OKAZ/) OKAZAKI T.
(OKAZ/) OKAZAKI T.
                                                                                                                                        generate
Sequence
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Sequence 337 BP; 104 A; 53 C; 59 G; 110 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   somatic gene therapy; ds.
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Fragment of centromere from human chromosome 21.
CENP-B box; mammalian artificial chromosome; MAC; chromosome 21;
mammalian telomere; centromere; yeast artificial chromosomes; YAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENP-B box sequences
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Mammalian artificial chromosomes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cooke HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V24222 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-1998.
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Local Similarity 100.0%;
see 9; Conservative
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                                           Similarity
                                                                                                                                            transgenic mice.
338 BP; 103
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                                       100.0%;
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                                       DB 43; L
1.37e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PT Manmalian artificial chromosomes - prepared using DNA construct PT comprising mammalian telomere and centromere containing copies of PT CENP-B box sequences
Disclosure; Page 57; 95pp; English.

Disclosure; Page 57; 95pp; English.

CC used in the DNA construct of the human chromosome 21 centromere, and can be CC used in the DNA construct of the invention. The construct is a mammalian cC artificial chromosome (MAC), and comprises a mammalian telomere and a CC entromere, where the centromere has a DNA sequence containing copies of the CENP-B box sequence. The invention also relates to methods for CC establishing yeast artificial chromosomes (YACs) comprising mammalian CC enteromeres. The method can be used to construct, modify CC and stably maintain YACs in yeast cells which have the ability to form CC MACs when introduced into mammalian cells. The MACs can be used for basic studies on CC enteromously, be stably maintained extrachromosomally and transmitted CC efficiently in mammalian cells. The MACs can be used for basic studies on CC conganisation and function of mammalian chromosomes and also as a vector CC construct to variable expression due to interest to test their functions in CC cause unpredictable insertion mutation on host chromosomes. Furthermore CC MACs will have the capacity to accommodate a DNA segment up to megabases CC where an entire large gene or group of genes and regulatory elements CC could be included. The MACs can be used for somatic gene therapy or to
                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Best I
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                                                                             01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                               Human gene signature HUMSS01120.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   generate
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-AuG-1998 (first entry)
Fragment of centromere from human chromosome 21.
CENP-B box: mammalian artificial chromosome; MAC; chromosome 21;
mammalian telomere; centromere; yeast artificial chromosomes; YAC;
               Matsubara K, Okubo K; WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cooke HJ, Grimes BR, Ikeno M, Masumoto H, Okazaki
WPI; 98-216941/19
                                                (MATS/) MATSUBAR
(OKUB/) OKUBO K.
                                                                                                                               Homo sapiens.
W09514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 somatic gene therapy; ds.
                                                                                                                                                                                                                                                                 T19986 standard; cDNA to mRNA;
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26-AUG-1996; WO-J02381.
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                                                              MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic mice.
339 BP; 103
 gene signatures
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3'-directed human cDNA library -
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132 ttctcagaa 140

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RESULTANCE OF THE PROPERTY OF 
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                                                                                                                           PT Modifying potatoes to form amylopectin starch - using an anti-sense construct to inhibit granule-bound starch synthase PS Claim 1; Page 21; 46pp; English.

CC A genomic library in EMBL3 was prepared using leaves of the potato Bintje. The library was screened with CDNA clones for the 5' and 3'.

CC ends of the GBSS gene. A full-length clone of potato GBSS gene was cidentified (wx311). An EcoRI fragment ("w")of the clones was found to contain the start of the gene and was cloned in pUCl3 to give pSw.

CC cloned in pUCl3 to give 19NH35. Further restriction of 19NH35 with SC cloned in pUCl3 to give 19NH35. Further restriction of 19NH35 with SC translation start and the first 125bp of the coding region. The C translation start and the first 125bp of the coding region. The C fragment can be used to make antisense constructs to suppress amylose formation in potatoes. See also Q26401-4.

Sequence 342 BP; 85 A; 78 C; 54 G; 125 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 529; 2245pp; Japanese.

Claim 1; Page 529; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. Codouble-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of the following period of the following construction of the GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-directed cDNA was initiated from the construction of mRNA by using poly(T) as the sole primer. Since the 3'-directed cDNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs, each library can be constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for ceograpising different cell types.

So Sequence 339 BP; 107 A; 63 C; 51 G; 116 T;
Query Match
Best Local S
Matches
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GBSS gene fragment I from potato.

Granule-bound starch synthase; amylopectin; amylose production;
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                          n 100.0%;
Similarity 100.0%;
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; SE-004096.
       Conservative
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Score 9;
Pred. No.
0; Misma
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                                         DB 4; Lo
1.37e+03
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Q60547;
New DNA sequences isolated from endogenous human retroviral element - and related vectors, transformed cells, proteins and antibodies, useful for diagnosis, treatment and prevention of breast cancer claim 11; Page 65; 173pp; English.

V68999 to V69038 represent nucleotide sequences which encode polypeptides used in detecting human breast cancer. Detection or measurement of human breast tumour specific polypeptides and nucleotide sequences, or the corresponding RNA in a sample, is used for diagnosis and monitoring of breast cancer. Human breast tumour specific polypeptides and nucleotide sequences, and the vectors containing the DNAs, are also useful in vaccines for inhibiting development (for prevention or therapy) of breast cancer. The polypeptides may also be used to raise monoclonal antibodies, used as immunoassay reagents.

Sequence 348 BP; 105 A; 60 C; 74 G; 104 T;
                                                                                                                                                                                                                                                                                                                                                     15-OCT-1998.
09-APR-1998; U06939.
11-DEC-1997; US-991789.
09-APR-1997; US-838762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                markers for human genes transcribed in-vivo, facilitate tagging of most human genes

Example 4: Page 351: 500pp; English.

The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated genes of care to facilitate
tagging of most human genes, for mapping locations of expressed genes
on chromosomes, for individual or forensic identification of tissue
locations of disease-associated genes, for identification of tissue
type, and for prepn. of antisense sequences, probes and constructs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA molecule encoding a polypeptide for detecting breast cancer #8 Human; breast cancer; breast tumour tissue; diagnosis; treatment; vaccine; epitope; endogenous; retroviral element; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams MD, Moreno RF, Venter WPI; 93-272882/34
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Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; s
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Human brain Expressed Sequ
Gene transcription product
                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP. Frudakis TN, Reed SG, Smith JM; WPI; 98-557473/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type, and for prepn. of antisense sequences, probes and const
EST02554 has a "poor" codding probability as evaluated using t
coding-region prediction program CRM. See also 059041-Q61440.
Sequence 343 BP; 91 A; 70 C; 95 G; 84 T;
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(USSH ) US DEPT HEALTH & HUMAN SERVICE
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| 25 ttctgagaa 33
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Local Similarity 100.0%;
les 9; Conservative
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. No. 1.37e+03;
Mismatches 0;
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Score

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Matches 9; Conservative
                                                                                                                                                              Homo sapiens.
W09316178-A.
19-AUG-1993.
12-FEB-1993; U01294.
12-FEB-1992; US-837195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity haematopolesis regulating activity, tissue growth activity, activiny. The estivity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, tumour inhibitio activity. Cadherin/tumour invasion suppressor activity, tumour inhibitio activity. The EST sequences are also stated to be useful for gene
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Expressed sequence tag;
tissue growth; activin;
                       Enriched oligonucleotides and corresp. sequences - used markers for human genes transcribed in-vivo, facilitate
                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICE Adams MD, Moreno RF, Venter CJ; WPI; 93-272882/34.
                                                                                                                                                                                                                                                                                                Human brain Expressed Sequence Tag EST01547.
Gene transcription product; genetic markers; tagging; in transcription; mapping; locations; chromosomes; chromosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q59805 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding human secreted proteins - de e.g. human blood, kidney, foetal lung, placenta, testes, ovary, pluttary, retina and colon cDNA libraries Claim 1; Page 467; 641pp; English.
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10-APR-1999; U06956.
10-APR-1997; US-837312.
(GEMY ) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg Racie LA, Spaulding V, Treacy M;
WPI; 99-070078/06.
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[larity 100.0%;
Conservative
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0; Mismatches 0;
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                                                                                              PT New nucleic acid encoding human chemotactic cytokine III - used for PT treatment of e.g. tumours, infections, autoimmune diseases etc. PS Claim 4; Pages 58-59; 73pp; English.

CC This DNA encodes the human chemotactic cytokine III (CCIII). The CCIII CC attracts and activates macrophages (or their precursors), neutrophils, CC basophils and some lymphocytes. This DNA is used to produce recombinant CCIII (including in vivo production) for treatment of CC conditions associated with CCIII like tumours, chronic or parasitic infections, leukaemia, T-cell mediated autoimmune disease, psoriasis, CC asthmal are growth factor activity, inhibit angiogenesis or promote wound the ling. Antagonists of CCIII are used to regulate haematopoiesis, CC for example, in glomerulonephritis, infections, autoimmune disease, CC HTLV-1 related disease, arthritis, infections, autoimmune disease, CC diseases, or susceptibility to them, can also be diagnosed by detecting mutations in the gene encoding CCIII, or by detecting abnormal levels of CCIII, e.g. using CCIII specific antibodies in usual immunoassays. The antibodies can also be used to identify or detect CCIII expressing clones and to purify CCIII. This encoding DNA is also useful for chromosome CC identification and for cloning the genomic sequence.

Sequence 371 BP; 67 A; 110 C; 112 G; 82 T;
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                                                Query Match
Best Local Similarity
                                    Matches
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The Expressed Sequence Tag was isolated from a human brain cDNA
library as part of a large set of ESTs which can be used as markers
for human genes transcribed in vivo. They can be used to facilitate
tagging of most human genes, for mapping locations of expressed genes
on chromosomes, for individual or forensic identification, for mapping
locations of disease-associated genes, for identification of tissue
type, and for prepn. of antisense sequences, probes and constructs.
See also 059041-061440.
Sequence 361 BP: 112 A; 74 C; 72 G; 101 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human chemotactic cytokine III (CCIII) encoding DNA. Chemotactic cytokine III; CCIII; human; treatment; t T-cell mediated autoimmune disease; leukaemia; psori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; W31512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 97-457539/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gentz RL, Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAR-1996; WO-U02
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30-мак-1998
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177 ttctcagaa 185
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33 ttctcagaa 25
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larity 100.0%;
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/note= "putative
142..300
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Pred. No. 1.37e+03
0; Mismatches
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leukaemia; psoriasis; asthma; ss.
                                                    DB 37; I
1.37e+03;
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RESULT 78

RESULT 78

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AC V89589 pt

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EST Clone CNS

KW Human; secret

KW Gree theray;

SO W99845456-A2.

PD 15-0CT-1998;

PO 15-0CT-1998;

PF 10-APR-1998;

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Claim 1; Page 266; 618pp; English.

The present sequence represents a human expressed sequence tag (EST). The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, hamantopolesis regulating activity, tissue growth activity, hamantopolesis regulating activity, tissue growth activity, hamantopolesis regulating activity, receptor/ligand activity, hamantopolesis regulating activity, receptor/ligand activity, hamantopolesis regulation activity, receptor/ligand activity, anti-inflammatory activity. activity. The polynucleotide may also be useful for gene therapy.

Sequence 374 BP; 100 A; 71 C; 85 G; 118 T;
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Best Local
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14-MAY-1998.
04-NOY-1997; U20520.
05-NOY-1996; US-743200.
(UYMA-) UNIV MASSACHUSETTS.
DOXSEY SJ;
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WPI; 99-07077/06.
New polynomia.
Screening for sclerotic disease in patients - anti-CP140 autoantibodies, altered CP140 mRNA, levels or an alteration in the CP140 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Partial nucleotide sequence from CP140 partial cDNA.

Partial centrosomal protein 140; CP140; cloning; screening; scleroderma;

Bluescript vector; anti-CP140 autoantibody; sclerotic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T. 79
V36486 standard; cDNA; 375
V36486;
28-SEP-1998 (first entry)
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tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                            P-PSDB; W61175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                  WPI; 98-286855/25.
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10-APR-1997; US-838821.
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "CP140 partial
/note= "no start or stop
sequence"
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Pred. No. 1.37e+03;
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CC The nucleic acids v36481-v36487 encode a variety of partial

CC polynucleotides from the partial centrosomal protein 140 (CP140) cDNA.

CC The CP140 partial cDNA was found by standard cloning and screening

CC The 1.7 kb cDNA was sequence was then subcloned into a Bluescript vector.

CC The 1.7 kb cDNA was sequenced and analysed and it was found that this

CC partial sequence contained one continous open reading frame. The

CC partial sequence contained one continous open reading frame. The

CC plynucleotides and polypeptides (W61170-W61175) can be used as a

CC diagnostic method for screening a patient for the presence of anti-CP140

CC autoantibodies as an indication of sclerotic disease. This can be

CC performed by taking a sample from the patient, adding to this a pure

CC cP140 fragment, and then seeing if any antibodies present will bind the

CC CP140 fragment. If any complexes are detected, it indicates that the

CC cp140 fragment is probably suffering from sclerotic disease.

SQ Sequence 375 Bp; 131 A; 83 C; 88 G; 73 T;
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Best Local S
Matches
                                                         The present sequence encodes a Helicobacter pylori cytoplasmic protein involved in genome replication, transcription, recombination and repair. The protein may be used in a voccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H. pylori cytoplasmic protein ORF 34574062.aa. Cytoplasmic; vaccine; prevention; treatment; infection; identification; vaccine; prevention; treatment; infection; bacteria; ir binding compound; bacterium; life cycle; activator; bacteria; ir duodenal ulcer disease; chronic gastritis; diagnosis; envelope; replication; transcription; recombination; repair; ds.
                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter Claim 9; Pages 265; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Berglindh OT, Smi
WPI; 97-052306/05.
isolated from H. pylori by PCR amplification for recombinant production, e.g. in E. coli hosts.

Sequence 381 BP; 96 A; 86 C. 01 C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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06-JUN-1996; U09122
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Local Similarity 100.0%;
nes 9; Conservation
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/note= "No stop
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Pred. No.
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-kag 0;
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Provary, pituitary, retina and colon cDNA libraries

Crossina sequence represents an expressed sequence tag (EST), and is

Crossina sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and colon suppressing activity, immune stimulating or suppressing activity, haematory conditions in the suppressing activity, haematory conditions in colon to the colon suppression activity, haematory conditions in colon to the colon suppression activity, the colon suppression activity, the colon suppressor activity the colon suppressor acti
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                     EST clone H0640.

Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
(GEMY ) GENETICS INST INC.

Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg Racie LA, Spaulding V, Treacy M;
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                                                                                                                15-OCT-1998.
10-APR-1998; U06956.
10-APR-1997; US-837312.
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10-APR-1998; U06956.
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d. No. 1.37e+03;
Mismatches 0;
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                                                               CC A single-stranded DNA (or its complementary strand or the corresp. CC double-stranded DNA) which comprises one of the 7837 "GS" sequences CC given in T19001-T26837 and which is able to hybridise to part of CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) CC sequences were obtained from 3'-directed cDNA libraries prepared CC from various human tissues; synthesis of cDNA was initiated from the C3'-enc of mRNA by using polly(T) as the sole primer. Since the 3'-CC untranslated sequence is unique to a particular mRNA species, almost CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library CC is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be C determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 413 BP; 99 A; 64 C; 75 G; 154 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PT e.g. human blood, kidney, foetal lung, placenta, testes, brain, provary, pituitary, retina and colon cDNA libraries
Claim 1; Page 515; 641pp; English.
CT he present sequence represents an expressed sequence tag (EST), and is care all secreted EST sequences isolated from a variety of human tissue courses. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for canimals, although no supporting data is given. Suggested activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, haemostatic and thrombolytic activity, receptor/ligand activity, tumour invasion suppressor activity, tumour inhibition activity, them suppressor activity, themetactivity, anti-inflammatory activity. The EST sequences are also stated to be useful for gene
Query Match
Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 95-206931/27.

Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-blased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 293; 2245pp; Japanese. A single-stranded DNA (or its comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 83
T19076 standard; cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene signature HUMGS00088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsubara K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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h 100.0%;
Similarity 100.0%;
9; Conservative
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Pred.
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e 9; DB 18; Le
l. No. 1.37e+03;
Mismatches 0;
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1.37e+03;
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detection;
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07-JUN-1994; EP-10869.
(GBFB ) GBF GES BIOTECH F
Collins J, Roettgen P;
WPI; 96-130768/14.
                                                                                                                                                                                                                                                          EP-699750-A1.
06-MAR-1996.
07-JUN-1995;
07-JUN-1994;
casseties were created by using the sequences represented by T15983-T15987 as amplification primers, and used to randomise the region coding the trypsin-inhibitory loop of pSKAN8. The products of these phagemids can be used to isolate phagemid particles with strong binding characteristics for defined target molecules, such as proteases (e.g. alpha-chymotrypsin or elastase). The phagemid particles can then be used to isolate protein ligands. The phagemid banks present a combined
                                                                                      Phagemid display banks expressing a fusion of a ligand and a fillamentous DNA bacteriophage protein - have defined target molecules such as protease(s), e.g. alpha-chymotrypsin or elastase example; Fig 1c; 19pp; English.

T15982 and T35865 represent fragments of the phagemid vector pSKAN8. T15982 and T35865 represent fragments of the phagemid vector pSKAN8. T15982 and T35865 represent fragments pancreatic secretory trypsin inhibitor (hPSTI) gene and the M13 pIII protein gene. In order to creat a randomised phagemid bank from pSKAN8, expression cassettes containing NNK repeats were created and inserted into pSKAN8. The expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; hPSTI; pancreatic secretory trypsin inhibitor; pIII protein; protease; vaccine; trypsin-inhibitory loop; alpha-chymotrypsin; elastase; antigen; M13; ss.
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/note= "binding :
200..222
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/note=
create
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                                                                                                                                                                                                                                                                                                                                                   /noté- "binding site for primer #1255 (see T15974)"
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/note= "pIII coding
407..414
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/note= "binding
343..393
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/product=
112..174
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15..37
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/note= "linker"
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187..218
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112..415
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full length pIII"
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                                                                                                                                                                                                                                                                                                                         join to T35685 to
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                  be used
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RESULT
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RESULT
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Disclosure; Fig 1d; 98pp; English.

This is the nucleotide sequence of subcloned fragment psgB23sp6 of the human uncoupling protein-2 (UCP2) gene present in genomic clone hUCP2-g1 (I-806). 10 subcloned fragments (see V44629-38) of hUCP2-g1 are provided. hUCP2-g1 was isolated from a human placenta genomic DNA library constructed in EMBL3 phage using mouse UCP2 cDNA as probe. psgB23sp6 is a non-localised fragment of the gene. The human UCP2 gene maps to a chromosomal region (11q13) linked to obesity and hyperinsulinaemia. The invention provides methods for the treatment of disorders associated with diminished or elevated UCP2 expression or activity. An agent which enhances UCP2 expression (e.g. an expression construct comprising a UCP2 encoding sequence) can be used to treat obesity, diabetes, syndrome X, hypothermia, hyperinsulinaemia, or glucose intolerance. An inhibitor of UCP2 (e.g. an antisense construct) is used to treat wasting, anorexia, inflammation, cachexia, fever or hyperthermia (all claimed). The invention also relates to diagnostic and drug
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22-APR-1997;
15-JAN-1997;

    py administering agent
effectively to treat obes

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Human uncoupling protein-2 gene clone hUCP2-gl sequence pSUB23sp6.
Human uncoupling protein-2; UCP2 gene; human; respiration;
Uncoupling protein-2; UCP2 gene; human; respiration;
thermogenesis; obesity; hyperinsulinaemia; glucose intolerance;
diabetes; syndrome X; hypothermia; wasting; cachexia; anorexia;
inflammation; fever; hyperthermia; gene therapy; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutational density and diversity in excess of that in similar banks, su as immunoglobulin presenting phagemids. Using the phagemids it is possible to produce antigenic components of vaccines in which only the mutated region is antigenic, the majority of the protein being a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYDU-) UNIV DUKE.
Bouillaud F, Collins SA,
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W09831396-A1.
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Local Similarity 100.0%;
hes 9; Conservative
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gening methodologies.
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                    standard;
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CALIFORNIA.
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gent which enhances or inhibits UCP-2 ac
obesity, diabetes, fever, hyperthermia,
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Mismatches 0;
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1.37e+03;
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PT DNA sequences representing aberrant forms of human high mobility provein genes - useful for treatment of endometriosis and proup protein genes - useful for treatment of endometriosis and provein genes - useful for treatment of endometriosis and provein for modulating vascularisation, etc.

PT tumours, or for modulating vascularisation, etc.

PS Claim 1; Fig 17; SBpp; German.

CV02880-V02898 are cDNA sequences that encode aberrant forms of the human child mobility group protein (HMG) gene, HMGI-C, which is located on chigh mobility group protein (HMG) gene, HMGI-C, which is located on chigh mobility group protein these protein binding domain. These proteins cantibodies derived from these proteins or expression modulators of the the translation product but not the proteins or expression modulators of the HMGI-C protein can be used in kits to modulate vascularisation and can improve vascular provision in myocardium damaged by infarction. Such proteins can also be used to treat endometriosis and tumours, for contraception (local or oral) and for tissue regeneration, especially in continues which are currently impossible or difficult to regenerate and the use of biological material with attendant risks of viral transmission and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      problem of proliferative arterial disease - using problems and treatment of proliferative arterial disease - using property of prolynucleotide(s), proteins and antibodies, e.g. to identify property inhibitors of RC-9 activity.

PS Claim 4; Page 19-20; 34pp; English.

RC-9 polynucleotides (T64806-09) correspond to partial, genomic and colMA sequences from rat, and human cDNA, respectively. The crat 424 bp partial genomic DNA fragment was isolated by differential display analysis of rat carotid arteries after balloon angioplasty and was used as a probe to isolate the genomic cangioplasty and was used as a probe to isolate the genomic canguence. RC-9 protein (see also W18513-14) is implicated in coronary arterial disease. RC-9 nucleic acids can be used in matches and coronary arterial disease. RC-9 nucleic acids can be used in coronary arterial disease. RC-9 nucleic and in the diagnosis and coronary arterial disease, and in the diagnosis and coronary arterial disease.
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use of biological material with attendant anaphylactic shock, is avoided. Sequence 430 BP; 129 A; 108 C;
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Human HMGI-C aberrant form 17.
High mobility group protein; HMGI-C; MAG; human; treatment; m multiple tumour aberration growth gene; vascular development; anglogenesis; vascularisation; endometriosis; contraception
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diagnosis; therapy;
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Rat RC-9 DN
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Arleth AJ, Autieri MV, Ohlstei
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Similarity 100.0%;
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in proliferative arterial disease diagnosis.
arterial disease; vascular restenosis;
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1. No. 1.37e+03;
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33 ttctcagaa

25

380 ttctcagaa 388

LT 88 V34161

standard; DNA; 436 BP.

(first entry)

protein gene 8

Human secreted 28-JAN-1999

Homo sapiens W09839446-A2

Query Match Best Local S

Watch 100.0%; Local Similarity 100.0%; Local Similarity 100.0%; es 9; Conservative

Score Pred. 0; M

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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1. No. 1.37e+03;
Mismatches 0
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The inventor relates to 70 novel genes and the secreted polypeptides they encode or by protein seguing to the pure to a human genes and treatment of e.g. cancers, neurological or disorders, immune diseases, inflammation or blood disorders

Claim 1; Page 170; 447pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. V34145) for increasing the stability of the fused protein as compared to the human protein only.

Compared to the human protein only.

The invention relates to 70 novel genes and their fragments (nucleic acid sequences: V34154-V34276; amino acid sequences W75057-W75179) which sequences: V34154-V34276; amino acid sequences W75057-W75179) which sequences: V34154-V34276; amino acid sequences w75057-W75179) which sequences by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypeptides, based on which tissues they are most highly expressed in (see V34154 for described conditions).
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P-PSDB; W75064.
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12-FEB-1992; US-837195.
(USSH ) US DEPT HEALTH & HUMA
Adams MD, Moreno RF, Venter C
WP1: 93-272882/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide cpds. with equine gamma interferon activity - are antivity antitumour and antisuppressive for use in horses.

Claim 18; Page 9; 39pp; German.

DNA was extracted from horse liver, digested and fragments isolated to be cloned in lambda phages. These were packaged in E. coli and tested with a human GI probe. A 4.6 kb BamHI fragment, encoding the entire gene was cloned in pUC9 to form pAHI11. The introns were removed from the corresponding mRNA and the fragments spliced to give a product which can be converted to "copy DNA".

The product is useful as antiviral, antitumour and immunosuppressive
of most human genes
Example 4; Page 191; 500pp; English.
The Expressed Sequence Tag was isolated from a human brain cDNA
library as part of a large set of ESTs which can be used as markers
for human genes transcribed in vivo. They can be used to facilitate
tagging of most human genes, for mapping locations of expressed gene
                                                                                                           markers
of most
                                                                                                                                                                                                                                                                                                                               16-MAR-1994 (first entry)
16-MAR-1994 (first entry)
Human brain Expressed Sequence Tag EST00528.
Gene transcription product; genetic markers; tagging; in vivo;
transcription; mapping; locations; chromosomes; chromosomal; ss.
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Q59535 standard;
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10-DEC-1986; DE-642096.
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llarity 100.0%;
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interferon polypeptide; antiviral agent;
ive agent; EGI; ss.
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1.37e+03;
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                                                                                                                                 tagging
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                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-and of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 450 BP; 111 A; 86 C; 110 G; 139 T;
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on chromosomes, for individual or forensic identification, for mapp locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST00528 has a "marginal" coding probability as evaluated using the coding-region prediction program CRM. See also Q59041-Q61440. Sequence 446 BP; 131 A; 100 C; 109 G; 106 T;
                                                                                                                                                                                                               V88140
V88140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsubara K. Okubo K;
WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T19056 standard;
T19056;
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A single-stranded DNA (or its comple
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(OKUB/) OKUBO K.
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                                                                                                                                                                                                                                           standard;
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Similarity 100.0%;
9; Conservative
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llarity 100.0%;
Conservative
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1. No. 1.37e+03;
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1. No. 1.37e+03;
Mismatches (
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PI Agostino MJ Jacobs K, Lavallie ER, McCoy JM, Merberg D,
PI Racie LA, Spaulding V, Treacy M;
PI Racie LA, Spaulding V, Treacy M;
PR New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT ovary, pituitary, retina and colon cDNA libraries

CC The present sequence represents an expressed sequence tag (EST), and is
CC The present sequence represents an expressed sequence tag (EST), and is
CC a polynucleotide of the invention. The polynucleotides of the invention
CC are all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences isolated from a variety of human tissue
CC contacting, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activitites
CC include nutritional activity, immune stimulating or suppressing activity,
CC and thrombolytic activity, chemotactic/bemokinetic activity, hammastatic
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene
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Best Local
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15-OCT-1992.
06-APR-1992: U02741.
05-APR-1991: US-681880.
(UYCO ) UNIV COLUMBIA NEW YORK.
AXE1 R, Buck LB;
WPI: 92-366257/44.
control insect populations or for detecting odours e.g. alcohol, explosives, natural gas etc.
Claim 19; Fig 24; 195pp; English.
The sequences given in 029855-77 are odorant receptor clones derived from an insect, a vertebrate, a fish or a mammal. These clones form a family of neurotransmitters and hormone receptors which transduce intracellular signals by activation of specific G-proteins. Each of these receptors is a member of a superfamily of surface receptors which traverse the membrane seven times. These clones are only expressed in the olfactory epithelium. These clones were isolated using probes derived from RNA prepared from the olfactory epithelia of Sprague-Dawley rats. Isolated cDNA's were amplified using primers which correspond to transmembrane domain 2 and 7. PCR products of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q29870;
Q29870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pheromone receptor clone JB Odorant receptor; insect; vertebrate; fish; mammal; neurotransmitter; hormone; G-protein; surface receptor; olfactory epithelium; PCR; Sprague-Dawley rat; amplify; primer; polymerase chain reaction;
                                                                                                                                                                                                                                  P-PSDB; R27882.
Nucleic acid encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                multigene family; ligand binding domain;
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10-APR-1998: U06956.
10-APR-1997: US-837312.
(GEMY) GENETICS INST INC.
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W09845437-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                   an odorant receptor -
tions or for detecting
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Pred. No.
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1.37e+03;
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e.g.
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alcohol,
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                                                                                                                                                              The present sequence encodes a secreted protein. The nucleic acid sequence is isolated from a human adult blood cDNA library using probe v63204. The polypeptide may have biological activities such has e.g. nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic activiny, inchemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, oadherin/tumour invasion suppressor activity, tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             appropriate size were isolated and sequenced. The deduced protein sequences of these CDNA's defined a new multigene family which shared sequence and structural properties with the superfamily of neurotransmitter and hormone receptors which traverse the membrane seven times. This novel family, however exhibits features different from any other member of the superfamily identified so far. There is striking divergence within the third, fourth and fifth transmembrane domains between the olfactory proteins. This divergence in the potential ligand binding domain is consistent with the idea that the family of molecules cloned is capable of associating with a large number of odorant of diverse molecular structure.

Sequence 481 BP; 85 A; 158 C; 92 G; 141 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-OCT-1998.
27-MAR-1998; U06176.
25-MAR-1998; US-823330.
28-MAR-1997; US-823330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; immune stimulating; suppressing; haematopoiesis regulating activity; tissue growth activity; activin; inhibin activity; chemotactic; chemokinetic activity; haemostatic; thrombolytic activity; anti-inflammatory activity; cadherin; tumour invasion suppressor activity; tumour inhibition activity; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V63193 standard; cDNA; 483
V63193;
13-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                   New isolated polynucleotide(s) and secreted proteins - are obtaine from human cDNA libraries prepared from adult testes, foetal brain, adult brain, adult blood and placenta Claim 25; Page 82; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      Agostino MJ, Jacobs
Racie LA, Spaulding
WPI; 98-542703/46.
                                                                                                                                   activity or other activities.
Sequence 483 BP; 156 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09844113-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA from clone eh61_1 which encodes a secreted
                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; W80409
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        , Lavallie ;
Treacy M;
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                                                                  Score
Pred.
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Pred.
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1. No. 1.37e+03;
Mismatches 0;
                                                                 re 9; DB 51; L
l. No. 1.37e+03;
Mismatches 0
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RESULT 95 ID V88491 standard; cDNA; 484 AC V88491;

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The EST sequences are also stated to be useful for gene
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W0985437-A2.
15-OCT-1998: U06956.
10-APR-1999; U06956.
110-APR-1997; US-837312.
(GEMY ) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie ER
Racie LA, Spaulding V, Treacy M;
New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries (Claim 1; Page 538; 641pp; English.

The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities
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Expressed sequence tag; secreted protein; haematopolesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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W09845437-A2.
15-OCT-1998.
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Agostino MJ, Jacobs K, Lavallie
Racie LA, Spaulding V, Treacy M;
WPI: 99-070078/06.
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V88866 standard; cDNA; 484
V88866;
12-FEB-1999 (first entry)
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10-APR-1997; US-837312.
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EST clone GS
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larity 100.0%;
Conservative
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Pred. No. 1.37e+03;
0; Mismatches 0
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Nuclear hormone receptor interacting polypeptides, esp. thyroid hormone-interacting proteins (TRs) for identifying proteins useful in treatment and diagnosis of thyroid related disorders by inoculating thyroid hormone receptor activity Disclosure; Page 42-43; 105pp; English.

A number of TR-interacting proteins have been isolated and their CDNA's partially sequenced. S112a gene shows no homology to any known gene and is shown in this sequence. Nearly all the fusion CDNAs isolated showed very strong dependence on hormone activation. The proteins can be used in an in vivo trap system for the isolation of proteins which associate with any nuclear hormone receptor. The proteins and Abs may be used to treat or diagnose thyroid disorders, and to modulate thyroid hormone receptor activity.

Sequence 495 BP; 152 A; 130 C; 98 G; 114 T;
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Q3-FEB-1995 (first entry)
Q3-FEB-1995 (first entry)
Parrial cDNA encoding S112a - a Tk-interacting protein.
Parrial thyroid hormone interacting proteins; TR; JL1; JL2;
parrial sequence; S112a; diagnosis; transcription factors;
transcriptional coactivator; treatment; thyroid hormone receptor;
thyroid related disorders; modulation; nuclear hormone receptor;
thyroid related disorders; disorders; modulation; nuclear hormone receptor;
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Q63681 standard; DNA; 495
Q63681;
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therapy.
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29-OCT-1993;
30-OCT-1992;
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Lee JW, MOOTE DD;
WPI; 94-199808/24.
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ttctcagaa
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larity 100.0%;
Conservative
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HOSPITAL CORP
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376..378
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/note= "stop
406..408
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1.37e+03;
                                                                     DB 11; I
1.37e+03;
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                                                                                 12-SEP-1991; A00419.
13-SEP-1990; AU-002294.
21-MAR-1991; AU-005175.
(CSIR) COMMONWEALTH SCIEN
(CSIR) Seow HF, Wood P
WPF; 92-150483/18.
P-PSDB; R23661.
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(GEHO) GEN HOSPITAL C
Lee JW, Moore DD;
WPI; 99-059040/05.
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V82582;
09-FEB-1999
Thyroid horm
                      DNA encoding ovine cytokine(s) cytokine(s) for treatment of immu Claim 2; Fig 1; 79pp; English.
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Ovis aries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells containing reporter gene construct
Disclosure; Fig 4; 69pp; English.
The present sequence encodes thyroid hormone receptor-interacting protein S112a. The protein was identified using the method of the invention. The method is used to determine if a test protein is cat of interacting with a nuclear hormone receptor protein in a ligand-dependent manner. The method is used especially to screen for proteins that interact with thyroid hormone receptors in a ligand-dependent or ligand-sensitive manner.

Sequence 495 BP; 152 A; 130 C; 98 G; 114 T;
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Q24293 standard; DNA; 498 BP
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02-APR-1992.
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US-969136.
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                                       immuno-depression in sheep
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new construct to express phytohormones in developing fruit useful for, e.g. producing substantially seedless fruit from transgenic plants
Disclosure; Page 35; 49pp; English.
This is the nucleotide sequence of the ovary-specific transcription regulatory element from the PLE36 gene of tobacco. A claimed DNA construct comprises either an isopentenyl transferase (see W81575) or a tryptophan oxygenase (see W81575)-encoding sequence, operably linked to an ovary or developing fruit-specific plant-expressible promoter (see also V69755 and V69759). The construct is used to stably integrate enzymes involved in cytokinin or auxin biosynthesis into the plant genome to achieve a transgenic plant (preferably nor auximber or watermelon) producing seedless fruit in the
                                                                                                                                                                                                                                                           Sequence
IFNX 416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1998.
06-MAY-1998; U09013.
06-MAY-1997; US-045725.
(UNIV ) UNIV KANSAS STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V69758;
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                                                                                                                                                                                                                                                                                                                                                                 N50023
N50023;
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                                                                                                                                            Homo
                                                                                                                                                                                  antiproliferative; ss.
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                                                                                                                                                                                                                 Antiviral;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cucumber or watermelon) producing seedless fruit in
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498 BP; 1
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llarity 100.0%;
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ding new modified human beta interferon polypeptides
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1.37e+03;
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EP-163993-A

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PresDB; p50022.

NR P-PSDB; p50022.

New modified human beta interferon polypeptide(s) - prepd. by p1 plasmid transformed bacteria, with improved antiviral, p1 plasmid transformed bacteria, with improved antiviral, p2 p1 anti-proliferative and immune regulating actions

PT anti-proliferative and immune regulating actions

PS Claim 28; Chart 2a, page 32; 7lpp; English.

CC compared with interferon beta prepd. by recombinant methods, the cC compared with interferon beta prepd. by recombinant methods, the p5 claim 28; chart inversion are more active and have different affinities cC for cell surface receptors (allowing selective targetting); they cc for cell surface receptors (allowing selective targetting); they call the preparation of the prepara
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17-MAY-1985;
17-MAY-1984;
                                                                                                                                                                                                                                                                                                New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions claim 28: Chart 2e, page 36; 71pp; English.

Compared with interferon beta prepd. by recombinant methods, the Compared with interferon beta prepd. by recombinant methods, the INFS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 112 A; 31 C; 67 G; 80 T;
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Bell LD, Boseley PG, Porter
WPI; 85-311944/50.
P-PSDB: PROPER
N50028 standard; DNA; 501 BP
N50028;
04-SEP-1991 (first entry)
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Bell LD, Boseley PG, Porter
WPI: 85-311944/50.
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N50027 standard;
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17-MAY-1984;
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                                                    New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions claim 28; Chart 2b, page 33; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the Compared with interferon beta prepd. by recombinant methods, the INFS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. sequence 501 Bp; 110 A; 32 C; 66 G; 81 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions claim 28; Chart 2f, page 37; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the Compared with interferon beta prepd. by recombinant methods, the INTS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 Bp; 114 A; 31 C; 68 G; 79 T;
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N50024;
04-SEP-1991 (first entry
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antiproliferative;
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17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
(SEAR) SEARLE G D & CO.
Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
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11-DEC-1985.
17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
(SEAR ) SEARLE G D & CO.
Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions claim 28: Chart 2c, page 34: 71pp; English.

Compared with interferon beta prepd. by recombinant methods, the INFS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. sequence 501 BP; 112 A; 30 C; 69 G; 85 T;
New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions (Claim 28; Chart 2) page 41; 71pp; English. (Compared with interferon beta prepd. by recombinant methods, the INFS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they
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N50025 standard; DNA;
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04-SEP-1991
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11-DEC-1985.
17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
(SEAR) SEARLE G D & CO.
Bell LD, Boseley PG, Porter
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Bell LD, Boseley PG, Porter
WPI; 85-311944/50.
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17-MAY-1984; GB-012564
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. No. 1.37e+03;
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WPI; 85-311944/50.
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P-PSDB; P50022.
Antiviral; cell growth regulator; antiproliferative; ss. Homo sapiens.
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11-DEC-1985.
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N50025 stand
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04-SEP-1991
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Compared with interferon beta prepd. by recombinant methods, the INFS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 Bp; 112 A; 31 C; 67 G; 80 T;
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Transforming growth factor-beta-receptor type II gene - useful for growth inhibition of cancer cells

Claim 2; Page 9; 12pp; Japanese.

T27596 is a cDNA sequence encoding the signal sequence and cytoplasmic domain of human transforming growth factor-beta (TGF-beta) receptor type II. The sequence was isolated from hepatoma cell line HepG2, and used as a probe for the isolation of the full coding sequence. The TGF-beta receptor is useful for inhibiting the growth of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions claim 28; Chart 2d, page 35; 71pp; English.

Compared with interferon beta prepd. by recombinant methods, the INFS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 108 A; 31 C; 70 G; 81 T;
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17-MAY-1985;
17-MAY-1984;
                                                                                                                               The gene is useful protein. Sequence 503 BP;
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17-MAY-1984; GB-012564.
(SEAR ) SEARLE G D & CC
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09-AUG-1994; JP-187031.
(SAKA ) OTSUKA PHARM CO
WPI; 96-174562/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-1996 (first entry)
Partial human transforming growth
TGF-beta receptor; anti-cancer; in
hepatoma; ds.
homo sapiens.
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Antiviral; cell growth
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T27596;
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inhibition; cytoplasmic domain;
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l. No. 1.37e+03;
Mismatches 0
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1.37e+03;
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                                                                                    Length 503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein genes - useful for frequent of encometrics and tumours, or for modulating various that encode aberrant forms of the human v02880-v02898 are cDNA sequences that encode aberrant forms of the human chiph mobility group protein (HMG) gene, HMGI-C, which is located on high mobility group protein (HMG) gene, HMGI-C, which is located on chromosome 12. These sequences encode the DNA binding part of the translation product but not the protein binding domain. These proteins, antibodies derived from these proteins or expression modulators of the HMGI-C protein can be used in kits to modulate vascular development. Such kits can reduce, block or stimulate angiogenesis or vascularisation and can improve vascular provision in myocardium damaged by infarction. Such proteins can also be used to treat endometriosis and tumours, for contraception (local or oral) and for tissue regeneration, especially in degenerating or damaged tissue. The regeneration method can be applied to use of biological material with attendant risks of viral transmission and canaphylactic shock, is avoided.

Sequence 506 BP; 167 A; 117 C; 124 G; 98 T;
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Best Local S
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21-DEC-1995; DE-048122.
(BULL/) BULLERDIEK J.
Bullerdiek J;
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
W09514772-A1.
01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1994; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene signature; messenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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High mobility group protein; HMGI-multiple tumour aberration growth angiogenesis; vascularisation; end
    tissues
Claim 1; Page 493;
A single-stranded I
                                                                                                                        Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA threflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                          Matsubara K, WPI; 95-2069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene signature HUMGS00997
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95-206931/27.
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Pred. No. 1.37e+03,
0; Mismatches (
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endometriosis; contraception
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3 directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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                                                                                                                                                              A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                      12.NOV-1998.

04-MAY-1998; U08985.

14-NOV-1997; US-066009.

16-MAY-1997; US-044031.

16-MAY-1997; US-044655.

(HUMA-) HUMAN GENOME SCI INC.

Barash SC, Dillon PJ, Kunsch CA;

MPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides

- used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis genome contig SEQ ID NO:388.
Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1571; 2084pp; English. A computer readable medium has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis.
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9; Conservative
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136 A;
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1.37e+03;
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PT New polynucleotides encoding human secreted proteins - derived from PT e.g. human blood, kidney, foetal lung, placenta, testes, brain, PT ovary, pituitary, retina and colon cDNA libraries
PT ovary, pituitary, regulate and colon cDNA libraries
PT ovary, pituitary, respective and sequence tag (EST), and is
CC a polynucleotide of the invention The polynucleotides of the invention
CC are all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences and proteins encoded by them are predicted to
CC cand useful biological activities which would make them suitable for
CC candinals, although no supporting data is given. Suggested activities
CC include nutritional activity, immune stimulating or suppressing activity,
CC haematopolesis regulating activity, tissue growth activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadharin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene.
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W09845437-A2.
15-OCT-1998.
10-APR-1998; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transglutaminase sequence and was isolated from a lambda-gtll human prostate tissue cDNA library using primers ZC4127 and ZC4129. This was done as part of the generation of a full-length human prostate transglutaminase cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST clone EP234.

Expressed sequence tag; secreted protein; haematopoiesis regulator; tagressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tunour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; trombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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Example; Page 36; 48pp; Engl
The sequence is that of the
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Q45770;
                                                                                                                                                                                                                                                                                                                                                                                                                     Agostino MJ, Jacobs K, Racie LA, Spaulding V, WPI; 99-070078/06.
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Degenerate; cellular apoptosis; enzyme; inter alia;
therapeutic wound repair; skin graft closure; food prepn.;
preparation; stabilising; marker; identifying agent; agoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1993
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W09313207-A.
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Local Similarity 100.0%;
hes 9; Conservative
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1991; US-816284.
ZYMOGENETICS INC.
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Pred. No. 1.37e+03;
0; Mismatches 0
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                      T98787 standa
T98787;
T98787;
10-NOV-1998
                                                                                                                                                                                                    This sequence includes the sequence of claim 1 (bases 319-477) modified by restriction sites for coupling to the beta-lactamase gene and insertion into plasmids. Beta-urogastrone can then easily recovered from the fusion protein expressed by transformants. The fusion protein is less easily degraded by proteases and so protects beta-urogastrone and beta-lactamase collects in the periplasm of E.coli. It is therefore easy to collect and purify the product. Beta-urogastrone is the hormone of the salvary glands which supresses stomach acid secretion and promotes cell growth, so is useful for treating ulcers and wounds. Previously the product was obtd. only in small amts, from human urine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-urogastrone - beta-lactamase
Beta-urogastrone gene; hormone; sa
fusion protein; beta-lactamase; ss
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Streptococcus
                                                                                                                                                                                                                                                                                                                              and transformed cells contg. it.
Disclosure: Page 59-61; 92pp; German.
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02-JUL-1984; JP-137691.
(EART-) EARTH CHEMICAL COL.
ACKL S. Obgai H, Horinaka A
            DNA encoding a S.
                                                                                                                                                                                                                                                                                                                                                               WPI; 86-015031/03.
P-PSDB; P60628.
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N60632 standard; DNA; 539 BP
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                                                                                                                                                                                                                                                                                                                                                     New gene for expression of beta-urogastrone -
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                                               standard;
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Similarity 100.0%;
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larity 100.0%;
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 a S. pneumoniae protein of unknown function.
pneumoniae protein; genetic immunisation; antagonist;
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The DNA sequences were isolated from Streptococcus pneumoniae strain colony (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and chivention can be used to identify compounds which interact with and control of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic in a mammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or T cell immune responses to protect the animal from disease. The croteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian cell invescillular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal implantation of in-dwelling devices or their than by the implantation of in-dwelling devices or other surgical techniques.

So sequence 541 BP; 136 A; 140 C; 91 G; 174 T;
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                                                                                                                                                                                                                                       Homo sapiens.

W09845328-A2.

15-OCT-1998.

09-APR-1997; US-991789.

11-DEC-1997; US-931789.

(CORI-) CORIXA CORP.

(CORI-) CORIXA CORP.
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Frudakis TN, Reed SG, Smith JM;
WPI; 98-557473/47.

New DNA sequences isolated from endogenous human retroviral element
and related vectors, transformed cells, proteins and antibodies,
useful for diagnosis, treatment and prevention of breast cancer
useful for diagnosis, treatment and prevention of breast cancer
seful for diagnosis, English.
15 Page 87; 173pp; English.
168800 to V68998 represent nucleotide sequences which encode human
breast tumour specific polypeptides. Detection or measurement of
                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JAN 1999 (first entry)
22-JAN 1999 (first entry)
DNA molecule encoding a breast tumour specific polypeptide #80.
Human; breast cancer; breast tumour tissue; diagnosis; treatment;
"""" Polypeptide #80.
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14-MAY-1997; U07950.
14-MAY-1996; US-017670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-1990;
15-FEB-1991;
21-JUN-1991;
                                                                                                                                                                                                                                                                adjuvant uses in animals
Disclosure; Fig 5D; 93pp; English.
Disclosure; Fig 5D; 93pp; English.
The inventors claim a DNA sequence coding for a polypeptide exhibiting ruminant cytokine or cytokine receptor activity; ovine interleukine (IL)-lalpha activity; ovine IL-1alpha activity; ovine tunour nectosis factor (NF) alpha activity; ovine interferon (IFN)-lambda activity; or interferon (IFN)-lambda activity; or ovine IL-2 activity or homologous sequences, derivs.
The recombinant polypeptides are also
                       Enterococcus faecalis genome contig SEQ ID NO:664. Enterococcus faecalis; contig; detection; Enterocovaccine; attenuation; computer readable medium; ds
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Q22834;
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X13601;
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                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequences coding for ruminant cytokine(s) or receptors - used for producing polypeptide(s) for therapeutic and/or
                                                                                                                                                                                                                                                                                                                                                                                                                         Brandon MR, Andrew WPI; 92-096916/12.
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t; immune response enhancer;
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A computer readable medium has been developed which has recorded on it properties of the computer readable medium has been developed which has recorded on it nucleotide sequences isolated from the Enterococcus faecalis genome. X1293 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
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04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
Claim 2; Pages 187-188; 333pp; English.

This sequence encodes a Streptococcus pneumoniae protein of unknown function. The invention provides DNA sequences (V65201 to V65304) from the Streptococcus pneumoniae genome and corresponding protein sequences (W80605 to W80728). A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the protein sequences. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in S. pneumoniae and for identifying viruience genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIL) LILLY & CO ELI.
Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas Mills BJ, Norris FH, Peery RB, Rockey PK, Rosteck PR, Skatrud PL, Smith MC, Solenberg PJ, Treadway PJ, Young Bellido ML; WPI; 98-348529/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding a S. pneumoniae protein of unknown function. Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip; virulence; antibody; infection; detection; treatment;
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Barash SC, Dillon PJ, Kunsch
WPI; 99-045171/04.
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1.37e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PT New polynucleotides encoding human secreted proteins - derived from PT e.g. human blood, kidney, foetal lung, placenta, testes, brain, presents, retina and colon cDNA libraries
PT ovary, pituitary, retina and colon cDNA libraries
PT ovary, pituitary, retina and colon cDNA libraries
PS Claim 1; Page 264; 641pp; English.

CC an polynucleotide of the invention. The polynucleotides of the invention of the present sequences isolated from a variety of human tissue of are all secreted EST sequences and proteins encoded by them are predicted to are useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and continuals, although no supporting data is given. Suggested activities conclude nutritional activity, immune stimulating or suppressing activity, haemostatic conditions in humans and the mematopolesis regulating activity, tissue growth activity, haemostatic activity, cadherin/tumour invasion suppressor activity, tumour inhibition contivity, cadherin/tumour invasion suppressor activity, tumour inhibition contivity, cadherin/tumour invasion suppressor activity, tumour inhibition
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Best Local S
Matches
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Best Local S
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                                                                                  10-JUL-1998 (first entry)

5' nucleotide portion of clone AS186_3.

Clone AS186_3; secreted protein; chromosome identification;

Identification; genetic disorder; nutritional use; cell proliferation;

cell differentiation; haematopoiesis regulating activity; tissue growtl

anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V88046;
                                                                                                                                                                                                                                                                                          V21154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy.
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMY ) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie
Raccie LA, Spaulding V, Treacy M;
WPI: 99-070078/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxia; chemokinesis, haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1998; U06956.
10-APR-1997; US-837312.
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W09845437-A2.
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||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                 25 ttctgagaa 33
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                                                                                                                                                                                                                                                                                              standard;
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Similarity 100.0%;
9; Conservative
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Similarity 100.08;
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   Location/Qualifiers 448..603
                                                                                                                                                                                                                                                                                                 CDNA;
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Pred. No. 1.37e+03;
0; Mismatches (
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Pred. No. 1.37e+03;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also stated to be useful
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RESULT 127
ID T28030;
AC T28030;
AC T28030;
DT 31-DEC-
DT 31-DEC-
DT MOUS SP.
FH Key
SW MMP typ
KW BMP typ
KW BMP typ
Cds
FT cds
FT cds
FT Cds
FT ROSE-
PR 04-NOV-
PR 05-JUN-
PR (PROC )
PI ROSE-DA
DR WFI; 96
DR P-ESDB,
FT Assays
FT Assay
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Matches
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26-FEB-1998; U14641.
20-AUG-1996; US-701931.
23-AUG-1996; US-701931.
(GEMY) GENETICS INST INC.
Jacobs K, Lavallie ER, McCo
Spaulding V, Treacy M;
WPI; 98-169159/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09614579-A1.
17-MAY-1996.
30-OCT-1995; U14027.
04-NOV-1994; US-334178.
05-JUN-1995; US-462467.
                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R95234.
Assays for bone
BMP type I recep
                           Disciosure; Page 79-80; 101pp; English.

A cDNA clone (T28030) codes for mouse incomplete bone morphogenetic protein (BMP) type II receptor kinase protein 3 (BRK-3) (R95234), corresponding to the extracellular, transmembrane and intracellular juxtamembrane region of full length BRK-3 (R95224). Host cells co-transfected with vectors carrying full-length, incomplete or soluble BRK-3 cDNA and full-length, incomplete or soluble BRF type I receptor kinase protein CDNA (see also T28018-29) express a BMP receptor complex useful for screening cpds. for BMP receptor affinity or for determining the concentration of a BMP receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the 5' nucleotide sequence of the c AS186.3. This clone is a full length clone, isolated from a human f kidney cDNA library, using methods which are selective for cDNAs encoding secreted proteins. The products of clone AS186.3 may as tissue/molecular weight markers, for chromosome identification, to identify possible genetic disorders, and to isolate new related They can also be used for nutritional uses, cytokine and cell proliferation, cell differentiation activity, immune stimulating or suppressing activity, haematopolesis regulating activity, thisbin activity, chemotactic/chemokinetic activity haematory activity, through the property activity activity, the constant activity, activity, the activity, receptor/ligand activity, anti-inflammatory activity, thmour inhibition activity or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-DEC-1996 (first entry)
Mouse incomplete BMP type II receptor kinase (BRK-3) cDNA.
BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;
BMP type I receptor kinase; BMP receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416 ttctgagaa
||||||||||
| 25 ttctgagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenbaum JS;
WPI; 96-251887/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth, haemostatic and thrombolytic Claim 18; Pages 45-46; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding secreted protein e.g. as immuno-modulators, anti-tumour
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llarity 100.0%;
Conservative
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/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAMBLE
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lators, anti-tumour agents,
and thrombolytic agents et
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1.37e+03;
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                                                                                                                                                                                                                                                                                                                                                 PT New polynucleotides encoding human secreted proteins - derived from PT e.g. human blood, kidney, foetal lung, placenta, testes, brain, provary, pitultary, retina and colon cDNA libraries.

PS Claim 1: Page 397; 618pp; English.

CC The present sequence represents a human expressed sequence tag (EST).

CC The present sequence represents a human expressed sequence tag (EST).

CC The polynucleotide, which is a secreted EST, and the encoded protein creating preventing or ameliorating medical human sand animals, although no supporting data is conditions in humans and animals, although no supporting data is CC given. Suggested activities include nutritional activity, immune cstimulating or suppressing activity, haematopolesis regulating cativity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.

SO Sequence 614 BP; 144 A; 149 C; 127 G; 194 T;
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Best Local S
Matches
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WO9845436-A2.

15-OCT-1998: U06955.

10-APR-1999; U5-838821.
                           3'utr
                                                     5'utr
                                                                                                                                           08-FEB-1996 (first entry)
Rat allograft inflammatory factor 1 (AIF-1) cDNA.
AIF-1; allograft inflammatory factor 1; transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS INST INC.
Agostino MJ. Jacobs K. Lavallie ER, McCoy
Racte LA, Spaulding V, Treacy M;
WPI: 99-070077/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; expressed sequence tag; EST; haematopolesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumou
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V89994;
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Q99370;
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1.37e+03;
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(HARD ) HARVARD COLLEGE.
RUSSell ME, Utans U;
WPI; 95-240668/31.
P-PSDB; R80521.
                                                                                                                                                                                                                                                                                                                       WO9636691-A1.
21-NOV-1996;
16-MAY-1996; U07025.
16-MAY-1995; US-4418.
08-APR-1996; US-6290
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(Sequence given in senucleotide 111 as C)
Sequence 627 BP;
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T43455;
08-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATM gene exon 15.

ATM gene; ataxia-telanglectasia; progressive genetic disorder; antibody; central nervous system; immune system; chromosomal instability; therapy; cancer predisposition; radiation sensitivity; cell cycle abnormality; multi-system disease; autosomal recessive; cerebellar ataxia; cerebellum; general motor dysfunction; Purkinje cell; oculocutaneous telanglectasia; ceresel; bulbar conjunctiva; facial skin; A-T; ss.
                  New isolated ataxia-telangiectasia gene - used to develop prods. for the study, diagnosis and treatment of ataxia-telangiectasia.

Claim 1; Page 60; 153pp; English.

743444-T43496 represent exons of the ATM gene of the invention.

Ataxia-telangiectasia (A-T) is caused by mutations, insertions, or deletions in the coding region of the ATM gene. A-T is a progressive genetic disorder affecting the central nervous and immune systems. A involves chromosomal instability, cancer predisposition, radiation involves chromosomal instability, cancer predisposition.
                                                                                                                                                                                                                          (KOHN/) KOHN K I.
(UYRA-) UNIV RAMOT APPLIED
Shiloh Y;
WPI; 97-012070/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding allograft rejection factors and immunogenic fragments useful for identifying transplant rejection inhibitors Claim 8; Fig 11a; 138pp; English.

Q99370 encodes the rat allograft inflammatory factor, AIF-1. The AIF-1 gene is a differentially expressed allograft gene which is expressed in allograft tissue during transplant rejection. Identification of the rat AIF-1 product (R80521) or transcript indicates that allograft rejection is taking place. The rat AIF-1 gand product are therefore useful in the diagnosis of transplant
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US-629001.
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18-AUG-1993;
05-NOV-1993;
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18-AUG-1994.
01-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 against influenza A and B Disclosure; Page 57-58; 151pp; English. A vaccine comprising an immunogenic fragment of the HA2 subunit of the influenza haemagglutinin (HA) protein from type A subtype IV and type B IV may be used for stimulating protection in animals against injection with influenza virus. The vaccine confers multi-strain immunity against strains IV A and IV B. The vaccines may be recombinantly produced, optionally as fusion proteins. Sequence 666 BP; 224 A; 118 C; 166 G; 158 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK) SMITHKLINE BEECHAM Dillon S, Kane J, Scott P WPI; 94-279392/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza haemagglutinin HA2 subunit coding sequence. Antigen; immunogen; vaccine; influenza; fusion protein; haemagglutinin; neuraminidase; flu; ds. H3N2 A/Victoria influenza virus.
Influenza haemagglutinin HA2 subunit coding sev
Antigen; immunogen; vaccine; influenza; fusion
haemagglutinin; neuraminidase; flu; ds.
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Q70205 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccines against multi strain influenza
                                                                                    30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; R60221
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Similarity 100.0%;
9; Conservative
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US-013415.
US-108914.
US-149150.
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                                                                                                                                           DNA:
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M, Shatzman
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Pred. No.
0; Misma
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d. No. 1.37e+03;
Mismatches 0;
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1.37e+03;
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ion protein;
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Claim 68; Fig 20; 220pp; English.

Craim 68; 220pp; 2
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Best Local S
Matches
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03-APR-1996; US-630916.
(CYTO-) CYTOGEN CORP.
(UYNC-) UNITY NORTH CAROL:
FOWIKES DM, KAY BK, PITO.
WPI; 97-503234/46.
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18-AUG-1994; U01149.
01-FEB-1993; US-013415.
18-AUG-1993; US-108914.
05-NOV-1993; US-149150.
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A vaccine comprising an immunogenic fragment of the HA2 subunit of the influenza haemagilutinin (HA) protectin from type A subtype IV and type B IV may be used for stimulating protection in animals against injection with influenza virus. The vaccine confers multi-strain immunity against strains IV A and IV B. The vaccines may be recombinantly produced, optionally as fusion protectins.

Sequence 666 BP; 223 A; 117 C; 167 G; 159 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H3N2
Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying cell signalling and growth regulatory polypeptides by
reaction with multivalent recognition complex - polypeptides are
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Pred. No. 1.37e+03
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17-NOV-1989; 001389.

8-DEC-1988; GB-028728.

8-DEC-1988; GB-09681.

27-APR-1989; GB-09681.

(KOCH-) Kochert Inst, (SANO) S.

Baggiolini M. Clemetson KJ, Wa.
LT 135
Q67599
Q67599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of specific WW domain interactions. The valency of the recognition units important in determining specificity of interaction with WW domains In multivalent form specificity is relaxed, but not lost, so proteins containing WW domains similar, but not identical, to the sequence of peptides' target WW can be detected, including new polypeptides. Sequence 673 BP; 199 A; 163 C; 170 G; 141 T;
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Q05141 standard; cDNA;
Q05141;
05-NOV-1990 (first eni
                                                                                                                                                                                                                                                                          as such is useful in treatment of bacterial, mycoplasma and viral infections. It is also useful in treatment of diseases, eg. psoriasis, arthritis and asthma.

Sequence 688 BP; 219 A; 149 C; 139 G; 181 T;
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psoriasis; arthritis; asthma; neutrophils;
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                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                         New neutrophil-activating peptide-2 - useful in treatment of infections and inflammatory conditions
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196..450
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No. 1.37e+03;
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1.37e+03;
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R 20-NOV-1993; US-979156.

R (TEXA) UNIV TEXAS SYSTEM.

Nucleic acid encoding retinoblastoma-associated polypeptide(s) - Noveleic acid encoding retinoblastoma-associated polypeptide(s) - Used for producing prods. for use in studying cell cycling and disregulated cell growth.

Pr used for producing prods. For use in studying cell cycling and disregulated cell growth.

Disclosure; Page 36; 77pp; English.

CDNA encoding a retinoblastoma (RB) associated protein (RAP), Apl2

CWAS cloned by direct screening of cDNA expression libraries using purified RB protein as probe. Apl2 showed transcription factor E2

CWAS cloned by direct screening of cDNA sequences were determined for Ap2 (067395, 067395, Ap8 (087397, 067398) and Ap15

CWAS cloned Ap10 (067601), which also encoded RB-associated
AU9347435-A.
23-DEC-1993.
17-SEP-1993;
22-DEC-1989;
02-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                               Q57506 stand
Q57506;
Q57506-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09412521-A.
09-JUN-1994.
19-NOV-1993;
20-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins.
Sequence
                                                                          gbo
                                                                                                       misc_signal
                                                                                                                                                                                                                                                                                                                                 Rat GAP-43 promoter. GAP-43; internal reg neuronal growth; pro
                                                                                                                                      misc_signal
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Retinoblastoma protein Api5 5' sequence.
Retinoblastoma-associated polypeptide; R
transcription factor; EF2; cell cycle; s
                                                                                                                                                                                                                                                                                                                      Rattus sp.
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Similarity 100.0%;
9; Conservative
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US-465635.
US-546453.
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546
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                                                     of GAP-43
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1.37e+03
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factor E2F
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10-APR-1992; O04406.
10-APR-1992; FR-004406.
(INRM ) INSERM INST NAT SANTE & F.
(INSP ) INST PASTEUR LILLE.
(INSP ) INST PASTEUR LILLE.
Capron A, Pierce R, Williams D;
WPI: 93-388582/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulate neuronal growth in animals, pref. humans Disclosure; Fig 14; 156pp; English. The nucleotide sequence of the rat GAP-43 gene promoter given in Q57506.
Sequence 700 BP; 230
                                                                                Claim 2; Page 10; 15pp; French.
The glutathione peroxidase is immunogenic diagnostic reagent and in the preparation sequence 720 BP; 233 A; 129 C;
                                                                                                                        P-PSDB: R44988.
Nucleic acid encoding schistosome glutathione peroxidase derived peptide, useful in diagnostic reagents and vaccin related vectors, transformed cells, etc.
                                                                                                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                Sequence encoding glutathione peroxidase. Glutathione peroxidase; Schistosomia mans diagnosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               Q53372;
03-JUN-1994 (first entry)
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(FISH/)
(STRI/)
(VALE/)
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Federoff HJ, Fishman
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                                        h 100.0%;
Similarity 100.0%;
9; Conservative
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         mansoni
  25
                                                                                                                                                                                                                                                                                            /note= "This stop codon is ignored due to a suppressor tRNA inserting a selenocysteine residue into the amino acid sequence.
                                                                                                                                                                                                                                                                                                                                    /product- Glutathione peroxidase 142..144
                                                                                                                                                                                                                                                                                   304..306
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1. No. 1.37e+03;
Mismatches (
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                                                   N 9
                                                                                                                                                                                                                                                                encodes Glutamic acid
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                                                                                                                                                                                                                                                                                                                                                                                                           mansoni; schistosome;
                                                  DB 9; Lt
1.37e+03
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                                                                                c and is used as n of vaccines.
146 G; 212 T
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RESULT ID V3

V34780

standard;

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RESULT
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New REI-Silencing Transcription factor (REST protein) - used therapeutically to control differentiation and activity of neural cells, e.g. in cases of brain cancer cells, e.g. in cases of brain cancer Claim 5; Page 40-42; 109p; English.

CA CDNA clone (T41404) codes for the DNA binding domain (R99364) of the human REST protein (see also R99355), or REI-silencing transcription factor, which inhibits expression of neural proteins in non-neural tissues by silencing promoters contg. REI elements (see also T41407). The cDNA sequence was derived from a full-length colone (T41406) coding for REST obtained. from HeLa cells. It can be used to produce REST DNA binding domain in transformed host cells, as a probe, and in gene therapy to treat conditions associated with excessive neural activity; antisense sequences can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local 9
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09-APR-1998.
06-OCT-1997; U18259.
06-OCT-1997; US-870815.
04-OCT-1996; US-726228.
(MILL-) MILLENNIUM PHARM I
GIMENO CJ. LEVINSON DA;
WPI; 98-240085/21.
P-PSDB; W59294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New activated T helper cell specific gene, RATH - used for developing products for treating e.g. autoimmune disorders, arthritis, graft rejection, asthma, allergy, infections or neoplasms Claim; Fig 2A-B; 127pp; English.

This sequence encodes a novel member of the human regulator of G-protein signalling (RGS) gene family, RATHI1. The encoded protein participates in the regulation, control and/or modulation of G-protein mediated signal transduction, involved in T cell activation, including T-helper (TH) cell and TH cell subpopulation activation. The protein can be used to develop products for treating autoimmune disorders, arthritis, graft rejection, asthma, allergy, infections or neoplasms.

Sequence 746 BP; 172 A; 217 C; 215 G; 142 T;
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Key
CDS
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22-MAR-1996; UC-409823.
23-MAR-1995; US-409823.
(UYNY) UNIV NEW YORK STATE RES FOUND Chong JA, Mandel G;
WPI; 96-443206/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human RATH1.1 DNA.

RATH1.1; RGS gene family; regulator of G-protein signalling; human; regulation; activation; modulation; signal transduction; T Cell; T helper cell; treatment; autoimmune disorders; arthritis; infection; graft rejection; asthma; allergy; neoplasm; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            Human REST protein DNA binding domain cDNA.
REST protein; REI-silencing transcription factor; neuron; neural cell; differentiation; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
W09629433-A1.
                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T41404;
13-JAN-1997 (first entry)
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11-SEP-1998
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Similarity 100.0%;
9; Conservative
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1. No. 1.37e+03;
Mismatches 0;
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                                                                                Haydock PV;
WPI; 96-200273/20.
WPI; 96-200273/20.
Detection of low copy number intracellular markers - by 3SR
amplification of target RNA in fixed cells then hybridisation
amplification of target RNA in fixed relication are a cervice in the control of target RNA in fixed relication are a cervice.
                                                                                                                                                  10-DEC-1991;
10-DEC-1991;
22-MAR-1994;
(DADE-) DADE
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     Example 2; Figure 3; 21pp; English.

An in situ hybridisation assay for detecting an intracellular marker of low copy number in cells comprises fixing the cells to a support using paraformaldehyde; treating the cells with a protease to permeabilise them without altering morphology; adding amplification reagents; incubating the cells at below fifty degrees celsius to perform amplification by self-sustained sequence replication; adding a labelled probe complementary to the region between the primers;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6/E7 region of Human Papilloma Virus 16 (HPV 16).
Human papilloma virus; HPV; detection; cervical ca
amplification; hybridisation; diagnosis; transform
                                                                                                                                                                                           US5506105-A.
09-APR-1996.
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                                                                                                  PT Recombinant virus vectors encoding human papillomavirus proteins presented by them, such as cervical cancer productions caused by them, such as cervical cancer productions caused by them, such as cervical cancer productions caused by them, such as cervical cancer products as a site for low plasmid pBR322/HPV16 (Durst et al., PNAS, 80: CC prepd. by PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: CC prepd. by PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: CC prepd. by PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: CC prepd. by sing oligonucleotides SO5 and SO6. The DNA prod. has a site for NcoI at the beginning of the E6 gene and a SmaI site commediately downstream of the termination codon for E7. The E6 and CC immediately downstream of the immortilising potential of E7 is removed by altering two key codons of the HPV E7 sequence. The single ORF of the PV-16 E6/E7 may be inserted into vaccinia virus DNA at neutral sites (pref. by inserting two sets of the DNA in opposite orientations to overcome the problem of intertypic recombination) to make a recombinant virus vector for use immunotherapeutically to activate cells of the formune system against HPV. See also Q23385-400 and Q29450-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Sequence 776 BP; 260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-1991; GB-005383.
(IMMU ) IMMUNOLOGY LTD.
Boursnell MEG, Inglis SI
WPI; 92-349219/42.
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Q29389;
Q9-MAR-1993 (fi
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10-МАК-1992;
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Pred. No.
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1. No. 1.37e+03;
Mismatches 0;
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PS Example 1; Page 83-84; 112pp; English.

CC The present sequence encodes a modified beta-lactamase (BL) used to CC exemplify the present invention. The present invention describes a method for identifying proteins or chemicals that directly or indirectly comodulate a genomic nucleic acid. The method comprises treating a living cell, which contains a BL-expressing construct integrated into a cell, which contains a BL-expressing construct integrated into a compound, then detecting BL activity in the cell. The method is used to identify chemicals such as drugs which are potentially used to treat immune responses; cardiac, vascular, neural, endocrine or gastrointestinal disorders; diabetes; obesity; inflammation; cancer and crauma. Generally the method is used to identify used to treat compound. The genome; modulators of these regions and cellular regions of the genome; modulators of these regions and cellular compounds. Measurement of BL provides rapid, in vivo, identification/ CC pathways. Measurement of BL provides rapid, in vivo, identification/ CC processes, and characterisation of these can be done in the same cells correction sustems.
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches
                                                V17983 standard; DNA; 795 BP.
V17983;
13-AUG-1998 (first entry)
Escherichia coli modified beta-lactamase DNA sequence SEQ ID NO Escherichia coli; Bacillus licheniformis; beta-lactamase; BL ge modification; identification; sensitive; rapid; cellular assay; drug discovery; modulator; immune response; diabetes; obesity; inflammation; cancer; trauma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1998 (first entry)
Escherichia coli modified beta-lactamase DNA sequence SEQ ID NO
Escherichia coli; Bacillus licheniformis; beta-lactamase; BL ge
modification; identification; sensitive; rapid; cellular assay;
drug discovery; modulator; immune response; diabetes; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-1997; U17395.
26-SEP-1996; US-719697.
(AURO-) AURORA BIOSCIENCES CORP.
Craig F, Foulkes GJ, Mere L, Neg
WPI; 98-230619/20.
                Synthetic.
Escherichia
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Escherichia coli.
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V17986 standard; DNA; 792
                                                                                                                                                                                                                                                                                                                                                                                                 screening system.
Sequence 792 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying modulators of genomic nuintegrated beta-lactamase construct
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02-APR-1998.
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33 ttctcagaa 25
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Similarity 100.0%;
9; Conservative
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Location/Qualifiers
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/transl_except= (pos:418..419,aa:Arg)
/note= "no stop codon given"
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Pred. No.
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. 1.37e+03;
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                                                                                                          gene;
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The present sequence encodes a modified beta-lactamase (BL) used to method for identifying proteins or chemicals that directly or indirectly modulate a genomic nucleic acid. The method comprises treating a living cell, which contains a BL-expressing construct integrated into a non-yeast eukaryotic genome, with a predetermined concentration of test compound, then detecting BL activity in the cell. The method is used to identify chemicals such as drugs which are potentially used to treat immune responses; cardiac, vascular, neural, endocrine or immune Generally the method is used to identify chemicals such as drugs which are potentially used to treat or gramma. Generally the method is used to identify useful/functional regions of the genome; modulators of these regions and cellular or pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways. Measurement of BL provides rapid, in vivo, identification/ pathways.
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14-MAY-1998.
27-OCT-1997; U19226.

01-NOV-1996; US-029930.

(SMIK) SMITHKLINE BEECHAM CORP.

(SMIK) SMITHKLINE BEECHAM PLC.

Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9813353-A1.
02-APR-1998.
26-SEP-1997; [
    New isolated nucleic acids from Streptococcus pneumoni
e.g. for identifying anti-bacterial(s) for treatment a
of meningitis
Claim 1; Page 112-113; 130pp; English.
The sequence is that of a coding region isolated from
s. pneumoniae. Its encoded protein, or agonists of it,
may be useful as an antibacterial for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae coding region. coding region; ORF; open reading frame; antibacterial; infection; prevention; meningitis; ss.
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Craig F, Foulkes GJ, Mere L
WPI; 98-230619/20.
P-PSDB; W48613
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26-SEP-1996; US-719697.
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integrated beta-lactamase construct
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Similarity 100.0%;
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/*tag=
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                                                                                                         acids from Streptococcus pneumoniae
anti-bacterial(s) for treatment and
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Pred. No. 1.37e-
0; Mismatches
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1.37e+03;
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                                                     밁
                                                                                                                                                                                                                            PT New chimeric enzymes, particularly for detection of analytes -
PT comprising a starting enzyme in which a mimetope is inserted to bind
PT a binding molecule to modulate the activity of the enzyme
PS Example 1; Fig 1B; 6)pp; English.

CC This sequence encodes a beta-lactamase fragment that can be used in the
CC chimeric enzyme (CE) of the invention. The CE comprises: (a) a starting
CC enzyme which is a polypeptide; and (b) a mimotope comprising at least one
CC amino acid, which mimotope is inserted into the starting enzyme or which
CC replacement yielding the CE which has an enzymatic activity of the:
CC starting enzyme and the activity of the CE is modulated upon binding of a
CC modulate the catalysis of a substrate by the CEs. The CEs can be used for
CC the detection of BMs which can be analytes such as an antibody specific
CC cerbB2, products of oncogenes, virus (e.g. HIV or hepatitis), or
CC cercia (e.g. Staphylococcus). Alternatively the CEs can be used for the
CC detection of ligands of the BMs.

SQ Sequence 817 BP; 215 A; 190 C; 227 G; 185 T;
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Best Local S
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                                                                                                                                                Query Match
Best Local
                                                                                                                       Matches
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V40858
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Beta-lactamase; chimeric enzyme; substrate catalysis modulator; c-erbB2; binding molecule detection; prostate specific antigen; PSA; CEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-1997; IB1643.
27-NOV-1996; US-757425.
(UYLC-) UNIV CATHOLIQUE LOUVAIN.
Fastrez J. Legendre D. Soumillion
WPI; 98-322712/28.
P-PSDB; W57890.
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Local Similarity 100.0%;
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ttctcagaa
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Similarity 100.0%;
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                                                                                                                                                   Score 9; DB 45; I
Pred. No. 1.37e+03;
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28-MAY-1998.
21-NOV-1997; U21347.
14-OCT-1997; US-061953.
22-NOV-1996; US-031626.
(HUMA-) HUMAN GENOME SCI INC.
(UYWI-) UNIV WISCONSIN.
Chol GH, Dillon PJ, Welch RA;
WPI; 98-312461/27.
                                                                                                                                                                                        US475549-A.
16-FEB-1988,
23-MAR-1984, 592714.
22-SEP-1980, US-189160.
23-MAR-1984, US-592714.
DNA coding for prolactin - obtd. by prepn. or reverse common for prolactin and inserting into a transfer vector. Claim 12: Fig 3: 10pp; English.
The cDNA was prepd. from RNA extracted from prolactin secreting tumours obtd. after surgical removal. The sequence can be inserted into expression vectors for the prodn. of prolactin which can be admin. to dairy cows to increase milk yield. It can also be used admin.
                                                                                                                                                                                                                                                                                                                                                                                                                          N80115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to elicit an immune response to pathogenic E. coli clid immune response to pathogenic E. coli strain J96 contig containing pathogenicity island (PAI) sequences, and represents a nucleic acid molecule of the invention. PAIs are large fragments of DNA which comprise pathogenicity determinants. The sequences of the invention are taken from PAI IV and PAI V. PAI IV is located at approximately 64 min (near phev) on the E. coli chromosome and is greater than 170 kb. PAI V is located at approximately 94 min (at pheR) on the E. coli chromosome and is greater than proteins encoded by the PAI open reading frames of the invention can be used in kits to detect uropathogenic E. coli. The proteins are used in vaccines to elicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1998 (first entry)
E. coli J96 pathogenicity island contig #36.
PAI; pathogenicity island: uropathogenic E. coli detection;
PAI V; pheV; vaccine; protective immune response; ds.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a protective immune response in an animal to the uropathogenic E. colistrain J96.
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P-PSDB; P82079.
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                                                                                                                                                             Cooke
                                                                                                                                                             (REGC) University of California Cooke NE, Baxter JD;
                                                                                                                                                                                                                                                                                                                                signal_peptide
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larity 100.0%;
Conservative
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88..684
/*tag= b
/label=prolactin
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               contraceptive; dairy cows;
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1. No. 1.37e+03;
Mismatches C
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See also
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein gene 4 clone HLTE125.
Human; secreted protein; fusion protein; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; lumnune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V84414 standard; DNA;
V84414;
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Similarity 100.0%;
9; Conservative
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US-048969

US-048915

US-048915

US-048972

US-049920

US-049920

US-057628

US-057647

US-057661

US-057661

US-057661

US-057661

US-057761

US-048971

US-057629

US-0577629

US-0577629
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PR 05-SEP-1997; US-057663.

PR 05-SEP-1997; US-057663.

PR 05-SEP-1997; US-057762.

PR 05-SEP-1997; US-057762.

PR 05-SEP-1997; US-048893.

PR 06-UNN-1997; US-057764.

PR 07-UNN-1997; US-057764.

PR 07-UNN-1997; US-057764.

PR 08-UNN-1997; US-057764.

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Query Match Best Local S Matches

h 100.0%; Similarity 100.0%; 9; Conservative

Score 9; Pred. No. 0; Misma

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pr having promoter and terminator derived from alcohol oxidase gene PS Claim 6; Page 22; 37pp; English.

CC An expression cassette which contains the alcohol oxidase promoter CC is induced when in the presence of methanol/glycerol. Under such CC conditions any heterologous gene located downstream of the promoter CC will be expressed. The expression cassette can be used to construct an expression vector which in turn can be used to transform cells. CC When transformed cells are cultured in the presence of methanol/ CC glycerol expression of the heterologous gene is induced such that CC large quantities of the desired product is produced. The CC large quantities of the desired product is produced. The CC craymes such as adenylate kinases, cytochrome C and peroxidases. CC The autonomously replicating sequence is used in the construction CC of the expression vector, conferring the ability of replication CC on the expression vector.

SQ Sequence 850 BP; 351 A; 83 C; 121 G; 295 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches
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Q48592;
DNA encoding maize acetyl coenzyme A carboxylase gene - used for prodn. of plants with herbicide tolerance or altered oil content claim 2; Page 92; 131pp; English.
6 Genomic DNA fragments (T39908-13) of maize Type A2 acetyl CoA carboxylase (ACCase) were isolated from a B37 genomic library by screening with a 2 kb subclone of cDNA clone #15-14 (see also T39904). Type A1 (see also T39904). Type A1 (see also T39904). Type A1 (see also T3904) by and Type B (T39914-16) genomic clones and a full-length cDNA clone (T39905) for ACCase (W05590) have also been obtd. ACCase sequences can be incorporated
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(SUNR ) SUNTORY LTD.
Hatanaka H, Kondo H, ;
WPI; 93-274483/35.
                                                                                                                                                                                                                                                                                                        Egli MA,
Wyse DL;
                                                                                                                                                                                                                                                                                                                                 05-APR-1995; US-417089.
(MINU ) UNIV MINNESOTA.
Egli MA, Gengenbach BG,
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10-OCT-1996:
04-APR-1996: U04625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JAN-1997 (first entry)
Maize acetyl CoA carboxylase Type A2 genomic clone F.
Acetyl CoA carboxylase; herbicide tolerance;
cyclohexanedione; aryloxyphenoxypropionic acid; vegetable oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycerol; yeast; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cea mays line B73
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                            PI assessed for enzyme expression

Example 1; Page 80-81; 112pp; English.

CC The present sequence encodes a modified beta-lactamase (BL) used to CC exemplify the present invention. The present invention describes a cc method for identifying proteins or chemicals that directly or indirectly comodulate a genomic nucleic acid. The method comprises treating a living CC enll, which contains a BL-expressing construct integrated into a cc non-yeast eukaryotic genome, with a predetermined concentration of test compound, then detecting BL activity in the cell. The method is used to identify chemicals such as drugs which are potentially used to treat cast cidentify chemicals such as drugs which are potentially used to treat compound, then detecting BL activity in flammation; cancer and crauma. Generally the method is used to identify useful/functional cregions of the genome; modulators of these regions and cellular regions of the genome; modulators of these regions and cellular completelis or chemicals associated with particular biological componence and characterisation of these can be done in the same cells componence and characterisation of these can be done in the same cells componence and characterisation of these can be done in the same cells contended to the same cells co
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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VI7984, v17984;
13-AUG-1998 (first entry)
13-AUG-1998 (fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AURO-) AURORA BIOSCIENCES CORP.
Craig F, Foulkes GJ, Mere L, Negulescu PA, Whitney MA;
WPI; 98-230619/20.
                                                                                                                                                                                                                                                                                                                                          Sequence
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Escherichia coli.
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                                        285 ttctcagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying modulators of genomic nucleic acid - using cell having integrated beta-lactamase construct exposed to test compound then
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26-SEP-1996; US-719697.
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ttctcagaa
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o stop codon given"
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RESULT 152 ID .V59591 standard; AC V59591;

DNA; 862

ВP

06-JAN-1999 (first entry)

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obsest; resteoclast; thymus; osteoprosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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                                                                                                                                                  몽
                                                                                                                                                                                    PT New isolated human genes and the secreted polypeptide(s) they encode provided for diagnosis and treatment of e.g. cancers, neurological providers, immune diseases, inflammation or blood disorders claim i, page 312; 721pp; English.

CC that in 1; page 312; 721pp; English.

CC the human cDNA clone HMMDN32 (deposited as clone ATCC 97900 and ATCC CC 209046) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin CC portion (e.g. V95902) for increasing the stability of the fused CC protein as compared to the human protein only.

CC The invention relates to 186 novel genes and their fragments (nucleic acid sequences: V5951-V59812; amino acid sequences W74731-W75026) which care useful for preventing, treating or ameliorating medical conditions ce.g. by protein or gene therapy. Also, pathological conditions can be CC diagnosed by determining the amount of the new polypeptides in a sample CC or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V59511 for described constitutions).
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18 16-JUL-1997; US-055874.

18 21-AUG-1997; US-055650.

22 -AUG-1997; US-056650.

22 -AUG-1997; US-056651.

22 -AUG-1997; US-056662.

23 -AUG-1997; US-056662.

24 -AUG-1997; US-056662.

25 -AUG-1997; US-056662.

26 -AUG-1997; US-056662.

27 -AUG-1997; US-056662.

28 22 -AUG-1997; US-056862.

29 -AUG-1997; US-056862.

20 -AUG-1997; US-056874.

21 -AUG-1997; US-056875.

22 -AUG-1997; US-056875.

22 -AUG-1997; US-056877.

22 -AUG-1997; US-056881.

22 -AUG-1997; US-056881.

22 -AUG-1997; US-056888.

22 -AUG-1997; US-056888.

22 -AUG-1997; US-056888.

22 -AUG-1997; US-056889.

23 -AUG-1997; US-056893.

24 -AUG-1997; US-056893.

25 -AUG-1997; US-056893.

26 -AUG-1997; US-056993.

27 -AUG-1997; US-056993.

28 -AUG-1997; US-056993.

29 -AUG-1997; US-056993.

20 -AUG-1997; US-056993.

20 -AUG-1997; US-056993.

20 -AUG-1997; US-056993.

21 -AUG-1997; US-056993.

22 -AUG-1997; US-056993.

23 -AUG-1997; US-056993.

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27 -AUG-1997; US-056993.

28 -AUG-1997; US-056993.

29 -AUG-1997; US-056993.

20 -AUG-
                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Sequence
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P-PSDB; W74811.
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11-APR-1997; 11-APR-1997;

06-MAR-1998 02-OCT-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 11-APR-1997 11-APR-1997

Homo sapiens. WO9839448-A2. 11-SEP-1998.

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Example 7; Fig 7D; 112pp; English.

CC This is the Type A2 ACCase genomic clone D partial nucleotide resistant corn CC This invention provides methods of preparing an herbicide resistant corn CC plant which comprises crossing a first corn plant to a second corn plant CC plant which comprises crossing a first corn plant to a second corn plant CC consistant allele and the second plant comprises at CC least 1 herbicide resistant allele which is not allelic to the herbicide resistant allele present in the first plant. The herbicide resistant corn CC plants are prepared using Accl and Acc2 gene combinations which impart CC cylcohexanedione (CHD) or aryloxyphenoxypropanoic acid (APA) herbicide tolerance to the corn plants and to produce CHD or APA herbicide tolerance to corn plants and to produce CHD or APA herbicide CC tolerant Zea mays (corn) homozygous or heterozygous for Acc2. The methods can also be used to CC carboxylase, selected from 3-(2,4-dichlorophenyl)-perhydroindolizine-2, CC candon, 3-isopropyl-6-(N-(2,2-dimethylpropyl)-acetamido-1,3,5-triazine CC -2,4 (1H,3H)dione, soraphen A and their structural analogues.

Sequence 867 BP; 240 A; 171 C; 198 G; 256 T;
N W09713323-A2.

N W09713323-A2.

10 22-MAX-1997.

F 18-NOV-1996; U19337.

R 16-NOV-1995; US-558666.

R 27-FEB-1995; US-725304.

R 21-OCT 1996; US-725304.

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A (ICOS-) ICOS CORP.

MPI; 97-289299/Z6.

R WPI; 97-289299/Z6.

R WPI; 97-289299/Z6.

T surveillance 1 alpha and beta proteins - useful for identify modulators and inhibitors for treating, e.g. ataxia telangie Example 8; Page 130; 212pp; English.
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29-AGG-1997; U15344.
30-AUG-1996; US-597826.
(MINU ) UNIV MINNESOTA.
(MINU ) UNIV MINNESOTA.
E911 MA, Gengenbach BG, Lutz SM, Mar
Somers DA, Vandee KL, Wyse DL;
WPI; 98-207043/18.
Herbicide resistant corn plants - pr
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Mammalian cell cycle surveillance 1; MCCS1; PIK-related kinase; phosphatidylinositol kinase; DNA repair; ataxia telangiectasia;
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V29323;
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16-SEP-1997
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                                                   useful for identifying .g. ataxia telangiectasia
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30-NOV-1992; BE0052.
29-NOV-1991; BE-001106.
(UYLO-) UNIV CATHOLIQUE LOUVAIN.
Fastrez J;
WPI; 93-197060/24.
P-PSDB; R37994.
                                                                                                                                       V22990; standard; cDNA; 892 BP.
V22990; y22990;
Q0-NOV-1998 (first entry)
Human p24 vesicle trafficking protein Hp24-2 nucleotide sequence.
ss; human; p24 vesicle-trafficking protein; endocrinal; cancer;
secretory disease; inflammatory disorder; gastrointestinal disorde
Homo sapiens.
Location/Qualifiers
CDS
88..777
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Q43705;
Q43705;
30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Selecting recombinant microorganisms expressing enzymes on t
surface - by affinity chromatography, using specific active
inhibitor, partic. for isolating phage(s)
Example; Fig 1; 45pp; French.

The nucleotide sequence of the gene for beta-lactamase on E.
plasmid pBR322 which is reproduced in Figure 1 is published
Sutcliffe, PMAS USA, 75, p. 3737 to 3741 (1987).

Sequence 890 BP; 238 A; 204 C; 229 G; 219 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A DNA sequence (172682) corresponds to a riboprobe generated from murine mammalian cell cycle surveillance 1 (MCCS1) DNA by in vitro RNA transcription. It was used to examine expression of MCCS1 (see also W19723-24) mRNA and protein in normal and irradiated mouse testes and in mouse embryos by in situ hybridisation. In both normal and irradiated mouse testes signal was observed in the cytoplasm of spermatogonia and spermatocytes. The expression level in irradiated testis was not increased over that seen in normal
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W09836068-A2.
20-AUG-1998.
12-FEB-1998; U02813.
14-FEB-1997; US-801740.
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Similarity 100.0%;
9; Conservative
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Similarity 100.0%;
9; Conservative
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0; Misma
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Pred. No.
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1. No. 1.37e+03;
Mismatches 0
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1.37e+03
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PT Genes involved in viral infection and tumour suppression - used to pri develop products for reducing or preventing viral infection or for suppressing tumours for reducing or preventing viral infection or for PT suppressing tumours for reducing or preventing viral infection gene. The present control of the sequence represents a viral infection gene. The present control of the invention comprise 70 viral infection (VI) genes and control of the invention comprise 70 viral infection (VI) genes and control of the serum protein (SP) allows selective elimination of cells control of the serum protein (SP) allows selective elimination of cells control of the serum protein (SP) allows selective elimination of cells control of the SP can be used for reducing or inhibiting a viral infection. Control of the TS gene products can be used to suppress a malignant control of the TS gene products can be used with viruse such as similar immunodeficiency virus, hepatitis virus or animal retroviruses such as communodeficiency virus, feline immunodeficiency virus, sequine infectious anemia virus, caprine arthritis encephalitis virus or visna virus.

Control of the identified genes are non-essential to cell survival, the control of the inventor of the control of the 
                                                                                                Query Match
Best Local
Matches
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Best Local
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15-APR-1996; US-015334.
(UYVA-) UNIV VANDERBILT.
Dubois RN, Organ EL, Rub
WPI; 97-526456/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human p24 vesicle-trafficking protein and related nucleic acid-
useful for diagnosis, treatment and prevention of e.g. cancer,
cystic fibrosis, diabetes etc.
Claim 22: Fig 2: 69pp; English
The human p24 vesicle-trafficking proteins and agonists, optionally
expressed in vivo from, are used to treat or prevent diseases associated
with abnormal vesicle trafficking, including endocrinal, secretory,
inflammatory or gastrointestinal disorders. Antagonists of human
p24, e.g. antisense nucleic acid, ribozymes, triplex-forming molecules,
antibodies, are used to treat or prevent cancers. Antibodies may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral infection gene SEQ ID NO:63.
Viral infection; tumour suppressor; cellular gene; rat; cancer serum protech; inhibitor; malignant phenotype; HIV; influenza; hepatitis; retrovirus; immunodeficiency; ds.
                                                                                                                                                                                                                       treatment m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp. w09739119-A1.
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                                                   495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 man O, Goli SK
98-467174/40.
ttctcagaa
                                                 ttctcagaa 503
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                                                                                                                    similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
Similarity 100.0%;
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892 BP; 268 A;
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                                                                                                                                                                                                                                            methods can be used in subjects without
                                                                                                                                                                                                the subjects.
911 BP; 274
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                                                                                             Score 9; DB 38;
Pred. No. 1.37e+03
0; Mismatches
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Pred. No. 1.37e+03
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                                                                                                                                                                                                  131 C;
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                                                                                                                                                 Length 911;
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IRESULT
ID OF THE PROPERTY OF 
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PT against influenza A and B
PS Example 10; Page 112; 151pp; English.

CA vaccine comprising an immunogenic fragment of the HA2 subunit of
CC the influenza haemagglutinin (HA) protein from type A subtype IV and
CC type B IV may be used for stimulating protection in animals against
CC injection with influenza virus. The vaccine confers multi-strain
CC immunity against strains IV A and IV B. The vaccines multi-strain
CC recombinantly produced, optionally as fusion proteins. NOTE: This
CS equence is a modified version of the sequence given in 070190,
CC having cytosine at positions 622, 625 and 634 instead of adenine, and
CC having thymine at positions 624, 627 and 636 instead of guanine.
CC These alterations are silent mutations i.e. the encoded polypeptide
CC the encoded H3HA2 protein.
CC Sequence 918 BP; 292 A; 179 C; 231 G; 216 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches
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18-AUG-1994; U01149.
01-FEB-1993; US-013415.
18-AUG-1993; US-108914.
05-NOV-1993; US-149150.
                                                                                                                                                                                                                                                                                                                                                                                DLT 159
Q70190 standa
Q70190;
Q8-MAR-1995
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Q70208;
30-MAR-1995
                                                                                                                                                                                                      haemagglutinin; neuraminidase; Influenza virus.
Location/Qualif cds 1.918
                                                                                                                                                                                                                                                                                              Sequence encoding immunogenic fragment of influenza haemagglutinin. Antigen; immunogen; vaccine; influenza; fusion protein; immunity; haemagglutinin; neuraminidase; flu; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM COULDINGS, KANE J. SCOTT M, WPI: 94-779392/34
P-PSDB; R60194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence encoding immunogenic fragment of influenza haemagglutinin. Antigen; immunogen; vaccine; influenza; fusion protein; immunity; haemagglutinin; neuraminidase; flu; ds.
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Influenza virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 918 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 100.0%;
Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471
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/product= NS1(1-81)H3HA2(1-221).
/note= "The sequence encodes a fusion prot-
which the N-terminal 81 amino acids are
derived from the influenza NS1 protein and
the remainder of the sequence is comprised
of amino acids 1-221 of the HA2 subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "The sequence encodes a fusion prote which the N-terminal 81 amino acids are derived from the influenza NS1 protein and the remainder of the sequence is comprised of amino acids 1-221 of the HA2 subunit of the H3HA2 subtype of influenza."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= NS1(1-81)H3HA2(1-221).
/product= nsi(1-81)H3HA2(1-221).
                                                                                                                                                                                                                              Location/Qualifiers
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Pred. No. 1.37e+03;
0; Mismatches of
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                                                                                        The present sequence represents a viral infection gene. The present CC invention describes nucleic acid sequences isolated from rat. The CC invention describes nucleic acid sequences isolated from rat. The CC sequences of the invention comprise 70 viral infection (VI) genes and CC absence of the serum protein (SP) allows selective elimination of cells cabsence of the serum protein (SP) allows selective elimination of cells cersistently infected with a virus from the cell culture. Inhibitors of the SP can be used for reducing or inhibiting a viral infection.

CC inhibitors of the TS gene products can be used to suppress a malignant cert of the SP gene products can be used with viruses such as HIV, influenza, hepatitis virus or animal retroviruses such as communodeficiency virus, avian immunodeficiency virus, bovine communodeficiency virus, feline immunodeficiency virus, equine infectious anemia virus, caprine arthritis encephalitis virus or visua virus.

CC because the identified genes are non-essential to cell survival, the creatment methods can be used in subjects without serious detrimental celeficits to the subjects.
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Best Local S
Matches
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Best Local Similarity
Matches 9; Conser
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Vaccines against multi strain influenza virus insection.

against influenza A and B

Glaim 23; Page 63-64; 151pp; English.

A vaccine comprising an immunogenic fragment of the HA2 subunit of the influenza haemagglutinin (HA) protein from type A subtype IV and type B IV may be used for stimulating protection in animals against injection with influenza virus. The vaccine confers multi-strain immunity against strains IV A and IV B. The vaccines may be recombinantly produced, optionally as fusion proteins.

recombinantly produced, optionally as fusion proteins.

295 A; 176 C; 234 G; 213 T;
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18-AUG-1994.
01-FEB-1994;
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18-AUG-1993;
05-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-1996; US-015334.
(UYVA-) UNIV VANDERBILT.
Dubois RN, Organ EL, Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon
WPI; 94
                                                                                                                                                                                                                                                                                                                                                                  suppressing tumours
                                                                                                                                                                                                                                                                                                                                                                                Genes involved in viral infection and tumour suppression - develop products for reducing or preventing viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral infection gene SEQ ID NO:43.

Viral infection; tumour suppressor; cellular gene; rat; cancer; serum protein; inhibitor; malignant phenotype; HIV; influenza; hepatitis; retrovirus; immunodeficiency; ds.
                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 62; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 97-526456/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9739119-A1.
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94-279392/34.
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larity 100.0%;
Conservative
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US-108914.
US-149150.
100.0%;
larity 100.0%;
Conservative
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Pred. No. 1.37e+03;
0; Mismatches 0
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 Mismatches
                 9; DB 38; Length 924; No. 1.37e+03;
                                                                  202 G;
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                      04-DEC-1997.
29-MAY-1997; U09194.
29-MAY-1996; US-632514.
                                                                                                                                         Apoptosis associated protein bbk gene.
Apoptosis associated protein; bbk gene; human; cell death;
Apoptosis associated protein; bbk gene; human; cell death;
cell proliferation; degenerative disorder; gene therapy;
Alzheimer's disease; autoimmune disease; cancer; inflammation;
                                                                                                                                                                                    T96064 standard; cDNA; T96064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
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amyloid precursor protein (NAP)
SPAP; amyloid precursor proteir
                         Gallo GJ;
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                                                                                                                                                                                                                                                                                                       Sequence
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         P-PSDB; W38358
                                                                                                variation
                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                       The SPAP
                                                                                                                                                                                                                                                                                                                               Disclosure; pp; English.
The gene product INS76, which is claimed as a senile plaque amyloid precursor (SPAP), has been shown to comprise four exons H, I, J and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N91055 standard;
                                                                      709745128-A1
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                  98-032326/03
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apoptosis associated protein
                                   APOPTOSIS
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                                                                                                                                                                                                                                                                                                       953 BP;
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i Kasei Kogyo.
Takahashi Y,
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157..158
/*tag= b
/note= "AAG
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/*tag= 8
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s of dysbolism in t
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Bbk
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1.37e+03
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Sequence 958 BP; 163 A; 314 C; 282 G; 199 T;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local
                                                            Transformed plant producing animal-derived anti-virus antibody easp. tobacco plants producing anti-tobacco mosaic virus monocional antibody

monocional antibody

Example 2; Pages 13-14; 26pp; Japanese.

Example 2; Pages 13-14; 26pp; Japanese.

O79929 and 079930 encode R66757 and R66758, the light and heavy chains of an animal derived anti-tobacco mosaic virus (TMV) monocional antibody. The cONAs were incorporated into a Ti plasmid vector, which was incorporated into A. tumefaciens. The resultant plant expression vector was used to transform tobacco plants, making them TMV resistant, the plants could also be biofarmed for the prodn. of anti-virus antibodies. Sequence 961 BP; 243 A; 255 C; 213 G; 250 T;
                                                                                                                                                                                                                                                                                         (NISB ) JAPAN TOBACCO I
(KURS ) KURARAY CO LTD.
WPI; 95-040220/06.
                                                                                                                                                                                                                                                                                                                                           22-NOV-1994.
07-MAY-1993; 131208.
07-MAY-1993; JP-131208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-tobacco mosaic virus monoclonal Ab light chain cDNA. Tobacco mosaic virus; TMV; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 163
Q79929 standard; cDNA to mRNA; 961 BP.
Q79929;
Q1-SEP-1995 (first entry)
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proliferation
Claim 11; Fig 2;
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Similarity 100.0%;
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34..93
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94..750
/*tag= c
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re 9; DB 14; Le
d. No. 1.37e+03;
Mismatches 0;
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AC V5
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DT Hu
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                                                                                                                                                                                                                                                                                                          PT Identification of cows giving high milk yields on basis of PT Identification of cows giving high milk yields on basis of PT Identification of exon 6 of PT-1 gene

SClaim 6; Fig 4; 22pp; English.

CC This sequence represents exon 6 of the bovine pituitary derived PTT-1 gene, showing the HinfI polymorphic site. This sequence was amplified CC using the primers given in T68930-31 for detecting the HinfI CC using the primers given in T68930-31 for detecting the HinfI CC using the primers given in T68930-31 for detecting the HinfI CC a genetype indicative of high milk production. The method comprises CC obtaining a nucleic acid sample from the bovine and ascertaining that CC the base at nuclectide position 165 in exon 6 of the bovine PIT-1 gene CC with HinfI, separating the resulting fragments, and ascertaining the term of the term of the primers are used to amplify the bovine PIT-1 gene CC pri-1 gene. These primers are used to amplify the bovine PIT-1 gene CC performed to detect an 800 bp fragment length polymorphism analysis is performed to detect an 800 bp fragment [indicating absence of a HinfI CC CC attle with the genotype are selected for breeding. The genotype CC lacking the HinfI site is associated with an average 13.2% increase in calk production and an average 11.2% increase in total protein.
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                                                                                                                                                                                                                                            Matches
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Best Local 9
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16-MAY-1994; 243543.
16-MAY-1994; US-243543.
(IOWA ) UNIV IOWA STATE R
FIEEMBAN AE, TUGGLE CK;
WPI; 97-201471/18.
P-PSDB; W18344.
JT 165
V59982 standard; cDNA to mRNA; 987 BP.
V59982;
V59982;
25-NOV-1998 (first entry)
Nucleic acid Tc2 encoding human homologue of rat acyl-CoA synthetase.
Human homologue; yeast RAD50; Drosophila Septin-2; Acyl-CoA synthetas
immunomodulatory activity; identification; activated T-cell; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine PIT-1 exon 6 sequence.
Primer; polymerase chain reaction; PCR; amplify; detection; RFLI
HinfI polymorphism; exon 6; bovine; pituitary; PIT-1 gene; genot
high milk production; restriction fragment length polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T68932 standard; DNA; 972 BP
T68932;
23-JUL-1997 (first entry)
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                                                                                                                                                                                                                                          Similarity 100.0%;
9; Conservative
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/note= "Encodes the last 70 amino acids of PIT-1"
complement (424..443)
/*tag= c
/note= "Binds primer given in T68930"
855..874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "Position of HinfI polymorphism"
468..678
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No. 1.37e+03;
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CC The sequence is that encoding a protein which can be used in the CC proteins BARDI, B123, BE2, BE14, BE31 or BE445, or a composition for the CC groteins BARDI, B123, BE2, BE14, BE31 or BE445, or a composition for the CC sequence, specifically a wild type BARDI composition for the CC risk of developing cancer. BARDI can be used in the preparation of an CC anti-BARDI antibody, and in the detection and purification of a BRCA1, BE31 or BE445 can used in the preparation of a BRCA1 binding protein agonist or antagonist that alters identification of a binding protein agonist or antagonist that alters CC identification of a binding protein agonist or antagonist that alters CC biological activity of the BRCA1-BARDI al23, BE2, BE14, BE31 or BE445 to BRCA1 or BE445 can used in the BE31 or BE445, a specific anti-BARDI, B123, BE2, BE14, BE31 or BE445, BE31 or BE445 can used to identify BE31 or BE445, a specific anti-BARDI antibody can be used to identify CC a patient having or at risk of developing cancer.
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BARD1; ring neric
                                                                                                                                                                                                                                                                                                                                            Baer R,
WPI; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human immunomodulatory poly:peptide(s) - have homology to the yeast RAD50 or Drosophila Septin-2 proteins
Disclosure: Page 64: 155pp: English.
V59981-89 represent mulitple isoforms of a human homologue of the rat brain long chain acyl-CoA synthetase. The present sequence has 90% overall homology to the rat gene, and is expressed in activated T-cells, testis, and foetal liver tissues. The specification also describes sequences encoding human homologues of the yeast RAD50, the Drosophila Septin-2 and Acyl-CoA synthetase. The proteins have immunomodulatory activity. The nucleic acids and proteins can be used to identify activated T-cells in a sample population. They can also be used to isolate and identify sequences
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WPI; 98-4
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03-APR-1997;
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27-FEB-1997; WO-U03159.
(GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                           P-PSDB; V54095.
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26-MAR-1998.
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Local Similarity 100.0%;
les 9; Conservative
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                                                                                                                                                                                                                                                                                                                                          R, Bowcock AM;
98-230317/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other proteins or other compounds having
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US-042985.
US-025296.
US-042611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
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No. 1.37e+03
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Claim 1; Page 28-30; 51pp; English.

Chaperone Firsy (W11328), which can be used to increase secretion of chaperone Firsy (W11328), which can be used to increase secretion of overexpressed proteins (homologous or heterologous) from Gram-

Compositive (esp. Bacillus) hosts. To isolate the gene, degenerate princers (see also T51351-53) were synthesized making use of existing the compositive (esp. Bacillus) hosts. To isolate the gene, degenerate compositive (esp. Bacillus) hosts. To isolate the gene, degenerate compositive (see also T1351-53) were synthesized making use of existing the composition of inversed PCR using a 110 bp fragment, which was composited from a nested PCR, a 4 kb fragment (see also 51356) was considered that included the firsy coding sequence. The gene can be concorporated into a recombinant vector pref. also conty, regulatory celements and opt. the gene encoding the protein of interest. By cleading the overexpressed protein into the secretion pathway, the composition and makes possible continuous culture and prodn. Sequence 1016 Bp; 346 A; 182 C; 252 G; 236 T;
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T51349 standard; DNA; 1016
T51349;
                                                                                                                                                        CTIA4-ova fusion protein encoding DNA.

CTIA4 receptor; CTIA4-Tg; fusion protein; B7 antigen; hinge; CH2; C extracellular domain; human; immunoglobulin; T cell; immune system; autoimmune disease; cancer; viral infection; ovalbumin; ss.
                                                                                                                                                                                                                                                                                              T 168
V69789 standard; DNA; 1021
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Broekhuizen CP, Kerk
WPI; 97-119052/11.
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     misc_feature
                                                                             sig_peptide
                                                                                                                                Homo sapiens.
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/note= "CD5 leader sequence"
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07-MAR-1996.
07-MAR-1995.
30-AUG-1995. AU0552.
30-AUG-1994; AU-007770.
07-NOV-1994; AU-009281.
(CSIR ) COMMONWEALTH SCI & IND RES ORG.
(AUSU ) UNIV AUSTRALIAN NAT.
BOEVINK PC, Chu PWG, Keese PK, Khan R1
Marshall US, Surin BP, Taylor WC, Water
WPI; 96-160363/16.
Circovirus transcription regulatory sequences and related constructs - useful in plants, esp. leguminous plants, for the modulation of gene expression

Glaim 4; Page 58; 121pp; English.

Claim 4; Page 58; 121pp; English

Claim 6; Page 58; 121pp; English

Claim 7; Page 58; 121pp; English

Claim 6; Page 58; 121pp; English

Claim 7; Page 58; 121pp; English

Claim 6; Page 58; 121pp; English

Claim 6; Page 58; 121pp; English

Claim 7; Page 58; 121pp; English

Claim 6; Page 58; 121pp; English

Claim 7; Page 58; 121pp; English

Claim 6; Page 58; 121pp; English

Claim 7; Page 58; 121pp; English

Claim 6; Page 68; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein of CTLA4 and immunoglobulin fragment - for treating immune system disorders
Example 8: Fig 26: 75pp; English.
This represents a nucleic acid sequence encoding a CTLA4-ova fusion protein. The invention provides a CTLA4-Ig fusion protein that binds the B7 antigen and has a first amino acid sequence consisting of the extracellular domain of CTLA4 and a second amino acid sequence consisting of the hinge, CH2 and CH3 regions of a human immunoglobulin molecule. The fusion protein inhibits interaction of T cells with B7-positive cells and may be useful for treating immune system diseases, e.g. autoimmune diseases, cancer or viral infections. The fusion protein encoded by the present sequence is an example of a soluble fusion protein and contains an amino-terminal CTLA4 domain and an ovalbumin carboxy-terminal domain. Sequence 1021 BP; 260 A; 246 C; 270 G; 245 T;
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01-DEC-1998;
18-JAN-1995;
18-JAN-1995;
27-JUN-1991;
22-JAN-1993;
28-MAY-1993;
15-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCSV; promoter; transcription; transgenic gene expression; crop improvement; ss. Subterranean clover stunt virus isolate F.
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Brady W, Damle NK, Ledbetter
WPI: 99-044666/04
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25 ttctgagaa 33
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Similarity 100.0%;
9; Conservative
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US-375390.
US-723617.
US-008898.
US-069693.
US-228208.
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/note= "s
449.1021
/*tag= c
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JA, Linsley
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1. No. 1.37e+03;
Mismatches (
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, Waterhouse PM;
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RESULT 170

ID V23014 standard; DNA; 1026 BP.

AC V23014;

C V23014 standard; DNA; 1026 BP.

AC V23014;

DT O5-AUG-1998 (first entry)
DNA encoding tryptophanyl tRNA synthetase of Streptococcus pneumoniae sp

ED DNA encoding tryptophanyl tRNA synthetase; trpS; Streptococcus pneumoniae sp

ED Streptococcus pneumoniae.

EH Key Clostridium longisporum; antagonist; treatment; inhibition; vac.

Streptococcus pneumoniae.

FH Key Clostridium longisporum; antagonist; treatment; inhibition; vac.

Streptococcus pneumoniae.

FH W09810652-Al.

10-MAR-1998;
11-SEP-1998; U16367.

PR 12-SEP-1996; GB-019072.

PR 12-SEP-1996; GB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae tryptophanyl tRNA synthetase - useful to pridentify drugs and raise antibodies for protection and diagnosis of streptococcal infection

PS Claim 4; Pages 8-9; 43pp; English.

Claim 4; Pages 8-9; 43pp; English.

CThe present sequence encodes a tryptophanyl tRNA synthetase (trpS) of streptococcus pneumoniae sp. 010093. This trpS is structurally related to other proteins of the tryptophanyl tRNA synthetase family. The protein exhibite greatest homology to Clostridium longisporum tryptophanyl tRNA competitive binding assays inhibit or activate trpS can be identified by competitive binding assays inhibit or activate trpS can be identified by competitive binding assays involving contact with the trpS protein. Antagonists can be used for treatment where inhibition of trpS is required. Disease related to trpS can be determined by determining the presence of nucleic acids encoding trpS in samples. TrpS can also be used to generate an immunological response in a mammal, by inoculation of trpS, adequate to produce antibody and/or T cell immune response to protect against disease.

So Sequence 1026 Bp; 323 A; 159 C; 239 G; 305 T;
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Best Local (
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V68168 standard; DNA; 1039
V68168;
15-FEB-1999 (first entry)
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                                                                                                                 antitumour;
Sus scrofa.
sig_peptide
                                                                                                                                      Interferon-beta 1; fibroblast antitumour; pig; ss.
                                                                                                                                                                                                   Porcine interieron-beta
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Similarity 100.0%;
9; Conservative
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     /*tag= 1
200..268
                                                          Location/Qualifiers 200..763
                                                                                                                                                                                                   CDNA.
                                                                                                                                                                                                                                                                                     BP.
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Pred.
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. 1.37e+03
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Best Local S
Matches
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19-MAY-1995; 444454.
02-OCT-1987; US-104461.
08-MAR-1982; US-355298.
01-NOV-1982; US-438128.
23-AUG-1991; US-749371.
21-SEP-1992; US-949327.
121-MAY-1995; US-944454.
(GETH) GENEWIECH INC.
Capon DJ, Goeddel DV;
                                                               19-MAY-1995; 446171.
02-OCT-1987; US-104461.
08-MAR-1982; US-395298.
01-NOV-1982; US-438128.
23-AUG-1991; US-749371.
21-SEP-1992; US-949327.
19-MAY-1995; US-446171.
(GETH) GENENTECH INC.
Capon DJ, Goeddel DV;
WPI; 98-593994/50.
                                                                                                US5827694-A.
27-CCT-1998.
19-MAY-1995;
02-CCT-1987;
08-MAR-1982;
01-NOV-1982;
23-AUG-1991;
21-SEP-1992;
119-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agents.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA sequence includes an open reading frame encoding porcine interferon beta-1 (see W83903). The invention provides bowine, murine, porcine, feline, laprine and rat mature alpha, beta and gamma interferons and their propeptides (see W83895-905, W83918 and W70582-85). Recombinant DNA methods can be utilised to prepare these non-human animal interferons in amounts sufficient to enable the determination of their biochemical properties and bioactivities, and hence to allow efficient production for commercial or biological and hence to allow efficient production for commercial or biological
                                                                                                                                                                                                              mat_peptide
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                                                                                                                                                                                                                                                                                                       Porcine interferon-beta 1 DNA. Interferon-beta 1; fibroblast
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P-PSDB; W83903.
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                      producing robioactivity
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V08185;
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           Claim 1;
                                                        P-PSDB; W73232
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 cDNA sequence
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Similarity 100.0%
9; Conservative
Fig 14B; 59pp; Eng:
A sequence includes
                             ing non-human interferon
  recombinant polypeptide(
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269..760
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1. No. 1.37e+03;
Mismatches 0
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                                polypeptide(s) .
(s) to determine
reading
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DE PRESENTATION DE LES DE L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence appears in the specification, but no further CC information is provided. The specification describes the production of CC artificial chromosomes. Artificial chromosomes can be produced by CC incorporating a DNA fragment comprising a selectable marker into a CC cells' genomic DNA, into or adjacent to an amplifiable region, and CC selecting a cell that comprises either a satellite artificial CC chromosome (8ATAC) (e.g. v04903-09), a de novo centromere, or a CC minichromosome (8ATAC) (e.g. v04903-09), a de novo centromere or a extra CC genomic locus for targeted integration of megabase size DNA fragments CC that contain single or multiple genes. SATACs can be introduced into CC embryonic cells of non-human animals to produce transgenic animals that corporate a heterologous DNA encoding a therapeutic product, e.g. anti-HIV. CT The DNA may also encode antigens that induce immunoprotective response CC gainst pathogen. These therapeutic products can be used in gene therapy. The artificial chromosomes are useful as cloning vehicles that accommodate entire genomes for the preparation of genomic DNA libraries, CC and also for the production of proteins which may be involved in a CC biochemical pathway or in multivalent vaccines.

SQ Sequence 1044 BP; 299 A; 184 C; 232 G; 329 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMERICAN GENE THERAPY INC.
(BIOL-) BIOLOGICAL RES CENT HUNGARIAN ACAD SC
(UYLO-) UNIV LOMA LINDA.
Hadlaczky G, Szalay AA;
WPI; 97-535860/49.
Producing satellite artificial chromosomes or useful for, e.g. cloning multiple proteins of multivalent vaccines, etc.
Example 12; Page 197; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-1997; U05911.
07-AUG-1996; US-695191.
10-APR-1996; US-629822.
15-UUL-1996; US-682080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          porcine, feline and rabbit mature interferons and their propeptide (see W73224-35). Recombinant DNA methods can be used to prepare these non-human animal interferons in amounts sufficient to enable the determination of their biochemical properties and bloactivities, and hence to allow efficient production for commercial or biological exploitation. Interferons are useful as antiviral and antitumour agents. A replicable expression vehicle comprising claimed non-human animal interferon nucleic acid, a process for producing such an interferon, and a microorganism (especially Escherichia coll) or cell culture transfected with the nucleic acid are claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-1998 (first entry)

Nucleic acid sequence of the specification.

Nucleic acid sequence of the specification.

Neo-minichromosome; multicentric; dicentric; chromosome; euchromatin; heterochromatic DNA; megachromosome; artificial chromosome; safakc; selectable marker; satellite artificial chromosome; SATAC; genomic loctargeted integration; transgenic animal; therapeutic product; gene therapy; cloning vehicle; genomic DNA library; chromosome fragmentation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interferon
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1039 BP;
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Score 9;
Pred. No.
0; Misma
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Pred. No. 1.37e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
   re 9; DB 38; Le
1. No. 1.37e+03;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome; SATAC; genomic locus;
therapeutic product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCI.
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a metabolic pathv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and their propeptides
                                                                   Length 1044;
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RESULT

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   FTH OK W DET ACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PT Polyniclectide encoding Streptococcus pneumoniae phenylalanyl trNA pr Polyniclectide encoding Streptococcus pneumoniae phenylalanyl trNA synthetase alpha and beta subunits - useful to diagnose, treat or prevent bacterial infection, especially meningitis

CC The present sequence encodes the alpha subunit of phenylalanyl trNA CC The polyniclectide encoding phes can be used for the recombinant CC production of phes, which can be used to treat conditions requiring phes CC control phes expression. Phes, or phes expressing vectors can be used to thirty. Sequences antisense to the polyniclectide can be used to conduct an immune response, i.e. an antibody (Ab) and/or T cell response, CC antivity, i.e. antibacterials. The antagonist, e.g. an anti-phes ab, can used to treat conditions requiring phes inhibition, e.g. an colling to the polyniclectide encoding phes or phes's concent for the polyniclectide encoding phes or phes's concent for the polyniclectide encoding phes and the polyniclectide encoding phes or phes's concent for the polyniclectide encoding phes and the polyniclectide encoding phes or phes's concent for the polyniclectide encoding phes and the phes can used as a probe to isolate full length correlated sequences, or diagnose, e.g. by polymerase chain reaction. CC e.g. by immunoassay. The Ab can used as a probe to isolate full length correlated sequences, or diagnose, e.g. by polymerase chain reaction. CC e.g. by immunoassay. The Ab can used to treat infection, isolate or claentify phes expressing clones, purify phes and as an immunoassay of mammalian cells and block the normal progression of infection. Sequence 1047 Bp; 284 A; 221 C; 261 G; 281 T;
                                                                                                                                                                                                                                                                                               RESULT
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Best Local
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23-OCT-1997:
18-APR-1997: U06876.
18-APR-1996: GB-007993.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
LAWLOR EJ;
WPI: 97-526215/48.
P-PSDB; W27668.
                                                                                     LT 175
Q57986 standard; DNA; 1060 BP.
Q57986;
20-AUG-1994 (first entry)
Genomic sequence of human CD8.
gp39; T-cell antigen; CD40 ligand; B-cell
gp39; fusion protein; CD8; fusion protein;
                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1027 ttctcagaa 1035
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Phenylalanyl trNA synthetase alpha subunit encoding DNA.
Phenylalanyl trNA synthetase; phas protein; bacterial in
meningitis; vaccine; antibacterial; immune response; ss.
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T88112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 100.0%;
Similarity 100.0%;
9; Conservative
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Location/Qualifiers 66..773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 9; DB 37;
Pred. No. 1.37e+03
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1047
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rigand for the CD40 receptor, causing proliferation and differentiation of B cells and some cancer cells PS Disclosure; Fig 9; 39pp; English.

CC The complete nucleic acid sequence of human gp39 (hgp39) protein CC (corresp. to cDNA) and the complete Ax sequence of hgp39 are CC presented in 057984 and R49548 respectively and contd. in plasmid CC CDM8-hgp39, deposited with the ATCC as E. coli, CDM8 Mc1061/p3-hgp39 CC and assigned accession No. 69050. The human T cell antigen gp39 is a CC ligand for the CD40 receptor. Soluble gp39 may be produced using the expression vector CD8-gp39. Chimeric genes may be constructed by GC fusing sequences encoding the extracellular domains of gp39 and CD8, pref. murine or human CD8 protein. Plasmid p3-shgp39 encoding the fusion protein of the extracellular domains from gp39 and CD8 pref. murine or human CD8 protein. Plasmid p3-shgp39 encoding the fusion protein of the extracellular domains from gp39 and CD8 Sequence 1060 BP; 196 A; 349 C; 204 C
     T coleopterans

Claim 5; Page 92-93; 139pp; English.

Claim 5; Page 92-93; 139pp; English.

C This DNA sequence encodes a novel soluble toxin (see W60228) of the Institute of Institute 
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Best Local
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09-MAR-1994:
03-SEP-1993: 114153.
04-SEP-1992: US-940605.
(BRIM ) BRISTOL-MYERS SC
AFULFO AAA, HOLLenbaugh
WPI: 94-076264/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9818932-A2.
07-MAY-1998.
30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-OCT-1997; US-029848.
30-OCT-1996; US-029848.
(MYCO ) MYCOGEN CORP.
Dullum CJ, Feitelson JS, Loewer D, Muller-Cohn J,
Dullum CJ, Feitelson JS, Loewer B, Muller-Cohn J,
Schnepf HE, Schwab G, Stamp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis Mīš-6 insecticidal toxin 19504 insecticide; pesticide; toxin; MIS-6; delta-endotoxin; biological control; lepidopteran; coleopteran; ss. Bacillus thuringiensis strain PS19604 (NRRL B-21860).

Key Location/Qualifiers
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V30311;
                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis toxins and nucleotide s
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                                                                                                                                                                                                                                                                                                                                                                   coleopterans
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Similarity 100.0%;
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Pred. No. 1.37e+03;
0; Mismatches (
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    used for producing pesticidal
for control of lepidopterans and

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                                                                                                                                PS Claim 4; Pages 201-202; 483pp; English.

PS Claim 4; Pages 201-202; 483pp; English.

CC This sequence encodes a Streptococcus pneumoniae protein that (based on CC homology with a Lactococcus lactis protein) is an anthranilate synthase CC component, and represents a DNA sequence of the invention.

CC 1010933 (NCIMB 40794). The Streptococcus pneumoniae proteins of the CC invention can be used to identify compounds which interact with and CC inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic cimmunisation. They can also be used to induce an immunological response consistation with the S. pneumoniae proteins or delivery CC of the encoding nucleic acids in a vector adequate to produce antibody CC and/or T cell immune responses to protect the animal from disease. The CC capable of inhibiting their bioactivity antimicrobial compounds which are CC capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian CC invention can be used to prevent adhesion of bacteria to mammalian CC progression of pathogenesis in infections initiated other than by the CC implantation of in-dwelling devices or other surgical techniques.

SQ Sequence 1087 BP; 314 A; 208 C; 264 G; 299 T;
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Matches
                                                                       Matches
                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a S. pneumoniae anthranilate synthase component. Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor. T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        including MIS-6, from B.t. isolates. MIS toxins are also under their ability to form pores in cell membranes, and can to facilitate entry of a second agent into a target cell. Sequence 1073 BP; 378 A; 193 C; 218 G; 284 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1997; U07950.
14-MAY-1996; US-017670.
(SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Streptococcus pneumoniae proteins diagnosing anti-microbial agents for tre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stodola RK;
WPI; 98-008793/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding a S. promistreptonocci
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                                    196
                                                                                      y Match 100.0%;
Local Similarity 100.0%;
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                                    ttctgagaa
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Similarity 100.0%;
9; Conservative
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                                                                   Conservative
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Pred. No.
0; Misma
                                                                                      Score 9;
Pred. No.
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1.37e+03;
                                                                                        1.37e+03
                                                                                                        DB 47;
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PS Claim 7; Page 47; 69pp; English.

CC This sequence represents the coding sequence for the rat UBCE2A cubiquitin conjugating enzyme) of the invention. The encoded protein catalyses the covalent attachment of ubiquitin to E2A. An anti-UBCE2A cantibody or a single stranded nucleic acid that is antisense to a portion of this sequence that reduces the level of UBCE2A biological activity in catalyses the used to inhibit the proliferation of a cell that expresses transcription factor E2A. The proliferation of a cell that expresses can inhibited by introducing a proteasome inhibitor into the cell or by introducing a proteasome inhibitor into the cell or cativator activity of wild type E2A but lacks the UBCE2A binding site or cacks at least 1 of the lysine residues which are ubiquitination sites on the wild type E2A.

So Sequence 1092 BP; 286 A; 264 C; 259 G; 283 T;
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Best Local S
Matches
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18-JUN-1998, U23224.

12-DEC-1997, US-989232.

11-DEC-1997; US-96523.

13-DEC-1996; US-766263.

(GEMY) GENETICS INST INC.

Agostino MJ, Jacobs K, Lavallie ER
Racie LA, Spaulding V, Treacy M;
WPI; 98-367424/31.
human adult (
libraries
Claim 17; Pag
This sequence
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V44860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone BG142_1 coding sequence. Secreted protein; nutritional source; cell proliferation activity; cell differentiation activity; immune stimulant; tissue growth activator; haematopolesis regulator; anti-inflammatory; tumour invasion suppressor; tumour inhibitor; clone BG142_1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HARD ) HARVARD COLLEGE. Haber E, Kho C, Lee M; WPI; 97-489625/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9735961-A1.
02-OCT-1997.
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Rat UBCE2A coding sequence.
Ubiquitin conjugating enzyme; UBCE2A;
transcription factor E2A; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Key
                                                                                                        New isolated
                                                                                                                                P-PSDB; W69241
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                             Page 68;
                                                                          d polynucleotides -
ovary, human adult
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larity 100.0%;
Conservative
  : 68; 108pp; represents a
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                             English
     polynucleotide
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ibitor; proteasome inhibitor; ds.
                                                                          obtained fbrain and
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an adult heart
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        invention,
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Matches
EP-621339-A.
26-OCT-1994; 302819.
20-APR-1993; JP-115216.
16-MAR-1994; JP-070194.
(TAKI) TAKARA SHUZO CO LTD.
Isegawa Y, Okuno Y, Sasao F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JLT 180
Q96139 standard;
Q96139;
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Sequence 1097 BP; 365 A; 209 C; 202 G; 321 T;
                                                                                                                                                                                                                                                                         072807;
22-JUN-1995 (first entry)
22-JUN-1995 (first entry)
DNA encoding stem region of A2/Aichi/2/68 influenza
Conserved peptide; stem region; hemagglutinin; HA; i
subtype; human; influenza A virus; immunogenic artii
antigen; vaccine; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               attenuated
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of prolactin or prolactin cDNA for enhancing the immune response of an animal to an infectious disease vaccine Claim 8; Page 14-15; 22pp; English.
A composition comprising prolactin or prolactin cDNA can be used for enhancing the immune response of an animal to an infectious disease vaccine. The composition can be used to enhance the effectiveness of vaccines which are considered "weak" e.g. bacterins and
                                                                                                                                                                                                                                                                                                                                                                                                                              T 181
Q72807 standard;
                                                                                                                                                                                                                                                       Human influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENZ ) GENZYME CORP
Kaplan J, Moscicki I
WPI; 95-292943/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prolactin; cDNA; vaccine; augment; bacterins; attenuated vaccine;
live vaccine; virus; immune response; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-1995.
14-FEB-1995; U01866.
14-FEB-1994; US-196350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    live vaccine; virus; 
Homo sapiens.
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5 ttctgagaa 33
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Similarity 100.0%;
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1100 BP; 324 A; 282 C;
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d. No. 1.37e+03;
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1.37e+03;
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29-MAY-1992 (first entry)
mglB-delta-alphalM fusion gene.
mglB-delta-binding protein; microglobulin;
Galactose binding protein; ms.
tubular kidney function; ss.
Location/Qualifiers
JLT 183
V30002 standard;
V30002;
V30002;
12-AUG-1998 (fi
DNA encoding a (
Sugar kinase; St
                                                                                                                                                                                                                                    The protein and antibodies to the protein are used for immunoassay of human microglobulin (for assessing tubular kidney function). See also Q21015-23.
Sequence 1112 BP; 310 A; 268 C.
                                                                                                                                                                                                                                                                                                   reptide with alpha-1-micro:globulin binding characteristics used in conjunction with specific antibodies for determining alpha-1 micro:globulin in body fluids alpha-1 micro:globulin in body fluids example 2.2; Page 9 + 20; 26pp; German.
Oligonucleotides 1-6 (Q21017-22) are used in the prodn. of alphalM(aa54-87)-alphalM(aa51-183). The ligated sequences form a 200 bp gene, which is inserted in the HindIII/BamHI pBR322 vector fragment (pBR322-delta-alphalM). The pBR322-delta-alphalM vector insert is then inserted into pVB1/EH to form pVB1/EH-delta-alphalM. Example 2.2 describes the prod. of galactose binding protein(aa1-306) application of the production of the protein pVB1/EH-delta-alphalM.
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This sequence encodes the stem region of the hemagglutinin (HA) molecule of the A2/Aichi/2/68 strain of human influenza A virus. This antigenim molecule contains the conserved peptides derived from the stem region of the HINI and HZNZ subtypes of human influenza A virus. Immunogenic polypeptides such as this are antigenically equivalent to the stem region the HA molecule of influenza A virus. This artificial peptide may used as a vaccine for prophylaxis of influenza A virus infection.

Sequence 1110 BP; 374 A; 216 C; 258 G; 262 T;
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01-APR-1998.
23-SEP-1997; 307424.
24-SEP-1996; US-027032.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
BURNHAM MKR, Lonetto MA, Warren PV
WPI; 98-208895/19.
P-PSDB; W56626.
                                                                                                                                                                                                                                                                                                                                                                                                     W09615222-A1.
23-MAY-1996.
15-NOV-1994; U13187.
15-NOV-1994; WO-U13187.
06-DEC-1994; ZA-009714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding staphylococcal sugar kinase - and corresponding sugar kinase polypeptide and antibody and antagonist claim 4; Pages 6-8; 36pp; English.

The present sequence encodes a sugar kinase of Staphylococcus aureus WCUH 29 strain NCIMB 40771. The specification describes products, compositions and methods for assessing staphylococcal sugar kinase expression, diagnosing and treating disease, e.g. infections of the upper respiratory tract, lower respiratory tract, heart, gastrointestinal tract, CNS, kidney and urinary tract, skin, bone and joint. The protein and nucleic acid may also be used to induce an immunological response
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                                                                                                                                         Human MutTs2 polypeptide - useful for hydrolysis and elimination of oxidised guanine nucleotide(s) to ensure correct DNA synthesis Claim 1; Figure 1; Sapp; English.

Mutated human MutT2 is implicated in diseases which are related to errors in DNA replication e.g. such as those which lead to tumours and cancers. Provision of wild type hmutT2 (especially by gene therapy) to patients allows oxidised guanine nucleotides to be
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T29786 standard; cDNA; 112,
T29786;
T7-DEC-1996 (first entry)
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Key Locati
CDS 1..111
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KIrkness EF, Wei Y;
WPI: 96-259830/26.
P-PSDB: R97739.
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08-APR-1997.
07-JUN-1995;
07-JUN-1995;
(MAYO-) MAYO
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15-MAY-1997; :
15-MAY-1997; :
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                                                                                                                     Example 3; Page 8-9; 15pp; Japanese. This sequence encodes the human decay accelerating factor (DAF) protein. DAF can be used in the viral vector of the invention. The viral vector contains a factor controlling the function of a human complement protein.
                                                                                                                                                                                                                                                                                                                                                                                                   DAF protein coding sequence.
DAF; decay accelerating fact
viral vector; ds.
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                                                        particularly a membrane combining type protein. The viral vector,
is stable in situ, is useful for gene therapy.
Sequence 1146 BP; 325 A; 277 C; 260 G; 284 T;
                                                                                                                                                                                                                    P-PSDB; W73505.
Vector having complement controlling
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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15-MAY-1997; JP-125965.
(DINA-) DINABEKKU KENKYUSHO
WPI; 99-074147/07.
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US-487810.
FOUNDATION.
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1.37e+03;
  DB 57; L
1.37e+03;
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uptake; kidney cell;
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P-PSDB: R67988.

Nucleic acids encoding CTLA4/CD28 counter receptor, Nucleic acids encoding CTLA4/CD28 counter receptor, for enhancing or suppressing T-cell mediated immune Claim 7: Page 106-107; 175pp; English.

Claim 7: Page 106-107; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W73639.

Fumour cell transfected to express B7-2 molecule - useful for tumour therapy by stimulating T-cell response placiosure; Column 31-34; 27pp; English.

This sequence encodes the mouse B7-2 antigen, which can be used in the method of the invention. The method is for transfecting an isolated mammalian tumour cell with an exogenous nucleic acid molecule encoding a mammalian B7-2 molecule, where the B7-2 molecule is expressed in the tumour cell is capable of costimulating a T-cell and is capable of binding a CD38 or CTLA4 ligand. The method is useful for treating tumours by stimulating a T-cell response against tumour cells in vivo.

Sequence 1151 BP; 353 A; 258 C; 255 G; 285 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 188
081366 standard: cDNA; 1163 BP.
081366; 21-AUG-1995 (first entry)
Murine B lymphocyte antigen B7-2.
B lymphocyte antigen; mB7-2; ss.
                                                                                                                                                          (REPK ) REPLIGEN CORP. Freeman GJ, Gray GS, WPI; 95-075236/10.
                                                                                                                                                                                                               (DAND )
(REPK )
                                                                                                                                                                                                                                        02-FEB 1995.

02-FEB 1995.

26-JUL-1994; U08423.

26-JUL-1993; US-101624.

19-AUG-1993; US-109393.

03-NOV-1993; US-147773.

(DAND ) DANA FARBER CANCER INST INC.
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03-NOV-1993; US-14773.
(DAND ) DANA FARBER CANCER INST INC.
Freeman GJ, Gray GS, Nadler LM;
WPI; 99-130394/11.
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V55785 standard; cDNA; 1151
V55785;
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| 33 ttctcagaa 25
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                                                                                B7-2 - useful responses
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S. pneumoniae. Its encoded protein or agonists of it,

S. pneumoniae. Its encoded protein or agonists of it,

c may be useful as an antibacterial for treatment or

c prevention of infection, specifically caused by S. pneumoniae

(c prevention of infection, specifically also Helicobacter

pylori (ulcers and gastric cancer). It may be of particular

(use before insertion of an in-dwelling device or any other

(c invasive procedure. The protein, or nucleic acid encoding

(it, can also be used in vaccines to induce a cellular

and/or humoral immune response, or to screen for other

(antibacterials. The DNA may also contain flanking sequences

that are potential sources of control elements for bacterial

gene expression. Detecting a sequence encoding the protein

c can be used diagnostically, e.g. to detect a mutation for

serotyping or classifying infectious agents.

Sequence 1167 BP; 385 A; 206 C; 247 G; 327 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA from activated M12 cells (a murine B cell tumour line).

COS cells were transfected with the M12 murine B cell library.

CDNA and screened for expression of B7-2. 6 clones were strongly positive. The B7-2 cDNA insert in clone 4 was sequenced in the positive. The B7-2 cDNA insert in clone 4 was sequenced in the positive. The B7-2 cDNA insert in clone 4 was sequenced in the positive. The B7-2 cDNA insert in clone 4 was sequenced in the positive common vector employing the following strategy. Initial sequencing was performed using sequencing primers T7 (081352) and common contains sequence obtd. Using these primers was used to design additional sequencing primers (see 081367-081370). The cycle cof sequencing and selection of additional primers was continued until the murine B7-2 cDNA was completely sequenced on both strands. A murine B7-2 cDNA was completely sequenced on both strands. A murine B7-2 cDNA was completely sequenced on both of the signal peptide would result in a murine B7-2 membrane bound protein having an unmodified mol. wt. of approx. 32 kDa. The extracellular domain contains nine potential N-11nked glycosylation sites. Glycosylation may increase the mol. wt. to about 50-70 kDa.

Except the sequence of the approx and a contains a contains a contains and the potential B8+ 1904 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
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Matches 9; Conservative
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Key
CDS
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V37401;
13-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acids from Streptococcus pneumoniae - useful. e.g. for identifying anti-bacterial(s) for treatment and preventic of meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                Reid RH, Zarfos PN WPI; 98-286586/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas
Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9819689-A1.
14-MAY-1998.
27-OCT-1997; U19226.
01-NOV-1996; US-029930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae coding region. coding region; ORF; open reading frame; infection; prevention; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mB7-2 clone 4 was deposited with the ATCC on August 18th Accession No. 69388.
                                                                                                                                                                                                                                                                                                                       Claim 1; Page 107-108; 130pp; English.
The sequence is that of a coding region isolated
                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W61013
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Pred. No.
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1.37e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                      of it,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RO
                                                                                                                                                                                                                                                                                                                                                                                      prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                  Monoclonal antibody against recombinant II-8 receptor polypeptide -
yr useful for treating inflammatory disorders, for detecting
neutrophil(s) and for isolating II-8 receptor from liq.mixt.

Disclosure; Fig 2A-B; 74pp; English.

Monoclonal antibodies were raised against recombinant interleukin-8
(II-8) receptor subtypes A and B from both human and rabbit sources
(R80950-53 encoded by 099949-52). The A subtype receptor (II-8rA) is a
low affinity receptor and the B subtype receptor (II-8rB) is a
low affinity receptor. The monoclonal antibody (mab) pref. binds to
the II-8 binding domain thus blocking its activation. The mabs are
useful for treating inflammatory disorders (see key words) and for
detecting the presence of neutrophils in a biological sample. The
mabs are also useful in the isolation of II-8 receptors from a mixture.

Sequence 1176 BP; 247 A; 333 C; 279 G; 317 T;
                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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15-MAR-1994; US-210250.
02-MAY-1994; US-237937.
(REPK ) REPLICEN CORP.
(UYBO-) UNIV BOSTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Key
cds
                                                                                                                                             V84163
V84163;
                                                                                                                                                                                                                            1108 ttctcagaa 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Witt DT;
WPI; 95-336945/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant high affinity interleukin-8 receptor subtype A encoding I1-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder; anabhylaxis; systemic lupus erythematosus; rheumatoid arthritis; systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;
            sig_peptide
                                                                  Key
                                                                               Streptococcus uberis.
                                                                                                       Streptococcus uberis plasminogen PauA; plasminogen activator; stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Greenfield EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9525126-A1.
21-SEP-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q99950 standard; DNA; 1176 BP.
                                                                                                                                  30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; R80951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adult respiratory distress syndrome; neutrophil detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 - APR - 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 833
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                                                                                                                                                                                                               ttctcagaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttctgagaa
||||||||||
                                                                                                                                                           standard; DNA; 1180 BP.
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                                                                                                                                (first entry)
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larity 100.0%;
Conservative
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      /*note= "this region 120..194
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                                                      120..
                                                                  Locat:
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                                                                 ion/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                 Score 9;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Navarro
                                                                                                      ogen activator protein Par
streptokinase; mastitis;
                                                                                                                                                                                                                                                                    Mismatches
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                           is specifically claimed in claim
                                                                                                                                                                                                                                                                              DB 17; L
1.37e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas
                                                                                                                                                                                                                                                                                          Length 1176;
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                                                                                                                    PauA
                                                                                                                   DNA.
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                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                 Gaps
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Best Local S
Matches
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09-MAR-1995.
05-AUG-1994; U09024.
13-AUG-1993; US-106016.
(IMMU-) IMMULOGIC PHARM CORP.
Griffith IJ, Kuo M, Lugman
                                                                                                                                                                                        cds
                                                                                                                                                                                                                                                                            02-NOV-1995 (first entry)
CDNA encoding Dac gV (clone 259).
Lolium perenne; Lol DV; Dactylis glome;
sensitivity; ryegrass pollen allergen;
                                                                                                                                                                                                                                                                                                                                          LT 192
Q85933;
Q85933;
                                                                                                             mat_peptide
                                                                                                                                          signal_peptide
                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (claimed) and other diseases and conditions by stimulating the production of anti-plasminogen activator antibodies, as pathogens use plasminogen activator to convert inactive plasmin in bovine milk to active plasmin, for use in growth. This is preferable to prior art methods using chemical antibiotics.

Sequence 1180 BP; 416 A; 199 C; 191 G; 374 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Streptococcus uberis plasminogen activator (PauA) polynucleotides and polypeptides - useful as diagnostic as vaccines to protect against mastitis caused by bacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP-887410-A2.
30-DEC-1998.
17-JUN-1998; 304759.
23-JUN-1997; US-050565.
                                                                                WO9506728-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PFIZ ) PFIZER INC.
Leigh JA, Rosey EL, Yancey
WPI; 99-047877/05.
                                                                                                                                                                                                                                                               Dactylis
                                                                                                                                                                                                                                                                                                                                                                                                                 556 ttctcagaa 564
|||||||||
33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 27-28; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W88239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
Local Similarity 100.08;
es 9; Conservation
                                                                                                                                                                                                                                                                                                                                                          standard; cDNA; 1181 BP.
                                                                                                                                                                                                                                                               glomerata.
                                                                                             /*tag= 0
125..961
/*tag= 0
                                                                                                                                                                     /note= "adaptor sequence'
53.964
/*tag= b
                                                                                                                                          /product=
1..124
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*tag c
/note- "this region is specifically claimed in 978..1088
/*tag- d
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                                                                                                                           ဂ
                                                                                                Q.
                                                                                                                                                          immature Dac gV protein
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Pred.
      3
                                                                                                                                                                                                                                                                                             glomerata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 60; I
1.37e+03;
                                                                                                                                                                                                                                                                                             Dac gV; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC claimed, encodes a new Streptococcus uberis planninogen activator, coting termed PauA (see W88239), that is involved in the development of mastitis in mammals. The pauA gene was amplified from S. uberis strain 95-140 chromosomal DNA using probes (see V84166-68) based on isolated peptides of PauA and by screening of transformant libraries for clearing activity on skim milk plates. A pauA gene was also polynucleotides are useful for recombinant production of PauA polypeptides. They are also useful for designing diagnostic primers and probes for detection of bacterial disease, including mastitis causing streptococci, particularly S. uberis, by amplification and detection of pauA polynucleotides (claimed). The PauA polypeptides are useful as vaccines to protect mammals against mastitis are useful as vaccines to protect mammals against mastitis the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inlium perenne Lol pv and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.

Example 5; Page 73-74; 110pp; English.

Example 5; Page 73-74; 110pp; English.

This is the cDNA sequence of clone 259, encoding Dac gV derived from a lambda gt10 library. The nucleotide sequence from 700 to 1181 is only preliminary and some bases may be misidentified (sic). Dac gV, isolated from Dactylis glomerata, is a major protein allergen related to ryegrass pollen allergens, eg. Lol pv. Peptides comprising at least one T cell epitope derived from the Lol pv. protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pv, such as
                                                                                                                                                                                                                                                                         New Streptococcus uberis plasminogen activator (PauA) polynucleotides and polypeptides - useful as diagnostic probes as vaccines to protect against mastitis caused by bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-1999 (first entry)
Streptococcus uberis plasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1132 ttctgagaa 1140
                                                                                                                                                                                                                            Claim 6; Page 30-31; 50pp; Enthis claimed polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                     EP-887410-A2.
30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V84164 standard; DNA; 1181
V84164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 95-115444/15.
P-PSDB; R71507.
                                                                                                                                                                                                                                                             infection
                                                                                                                                                                                                                                                                                                                            P-PSDB; W88240
                                                                                                                                                                                                                                                                                                                                        (PFIZ ) PFIZER INC.
Leigh JA, Rosey EL, Yancey
WPI; 99-047877/05.
                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-1998; 304759.
23-JUN-1997; US-050565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PauA; plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dac gV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1181 BP;
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/note= "this
979..1089
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196..978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
121..981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasminogen activator protein PauA DNA.
tivator; streptokinase; mastitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000
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                                                                                                                                                                                                                                           English
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Pred.
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0 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is specifically claimed
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1.37e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claim 5"
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RESULT
ID V5
AC V5
DT 25
DE NU
KW HU
KW 1n

25-NOV-1998 (first entry)
Nucleic acid Tcl encoding
Human homologue; yeast RAD
immunomodulatory activity;

! encoding huma
; yeast RAD50;
/ activity; ide

identification;

human homologue of rat acyl-CoA synthetase; D50; Drosophila Septin-2; Acyl-CoA synthetase;

V59981, V59981,

standard;

CDNA

to mRNA; 1189

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                           inhibitors, used for treating e.g. tumours, inflammation or traumatic or ischaemic injury

provided in the treating e.g. tumours, inflammation or traumatic; Page 52; 70pp; English.

A DNA molecule (T62556) codes for human IP-10 (W14307), a 10 kDa conceptor and which is capable of inhibiting endothelial cell proliferation. IP-10 nucleic acids can be used to prepare recombinant IP-10, esp. as a non-aggregating fusion protein with calkaline phosphatase as fusion partner. IP-10, or a nucleic acid cencoding it (provided e.g. by a viral vector), can be used to endotheliomas or arteriosclerosis, and to inhibit fibroblast endotheliomas or arteriosclerosis, and to inhibit fibroblast growth factor or transforming growth factor-beta activity.

Sequence 1185 BP; 389 A; 234 C; 210 G; 352 T;
                                                                              Query Match
Best Local
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                                                                  Matches
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Sequence 1181 BP; 415 A; 198 C; 193 G; 375 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IP-10 gene.

IP-10; chemokine; inhibitor; endothelial cell; endothelioma; IP-10; chemokine; sarcoma; sclerosing endothelial sarcoma; tumour; Karposi's sarcoma; sclerosis; inflammation; fibrosis; hemangioma; neoplasm; arteriosclerosis; inflammation; fibrosis; keloid; proliferative retinal disorder; traumatic injury; keloid; proliferative retinal disorder; traumatic injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                               Modulation of endothelial cell growth - using IP-10 or IP-10 inhibitors, used for treating e.g. tumours, inflammation or
                                                                                                                                                                                                                                                                                                                                                                                               Heder P, Luster A; WPI; 97-087169/08.
                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-1996; U10726.
22-JUN-1995; US-493638.
(HARD ) HARVARD COLLEGE.
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                                  731 ttctcagaa
 33 ttctcagaa
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                                                               h 100.0%;
Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                            Recombinant and isolated nucleic acids - encode enzymes and proteins involved in plant abscission or dehiscence. Disclosure; Fig 8; 39p; English.

The cDNA encodes a rape (cv. Rafal) protein involved in abscission or dehiscence, and can be used to manipulate plant abscission and reduce/prevent pod dehiscence, especially to regulate abscission or policy from anthers, to generate male sterile plants and for hybric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1993; GB-00672b.
31-MAR-1993; GB-00672b.
(NICK-) NICKERSON BIOCEM LTD.
CA. ISABC PG, ROBERTS JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     v59981-89 represent mulitple isoforms of a human homologue of the represent long chain acyl-coA synthetase. The present sequence has 90% overall homology to the rat gene, and is expressed in activated T-cells, testis, and foetal liver tissues. The specification also describes sequences encoding human homologues of the yeast RAD50, the Drosophila Septin-2 and Acyl-CoA synthetase. The proteins have immunomodulatory activity. The nucleic acids and proteins can be used to identify activated T-cells in a sample population. They can also be used to isolate and identify sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dolganov
WPI; 98-4
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Q73730 standard;
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26-APR-1995
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27-FEB-1997; U03159.
27-FEB-1997; WO-U03159
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WO9838306-Al.
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31-MAR-1994;
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es 9; Conse
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94-333203/41.
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  standard; DNA; 1204
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dehiscence; transgenic
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1.37e+03;
                                                                                                                                                                                                                                                                      218 G;
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and for hybrid
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04-NOV-1997; CA0829.
04-NOV-1996; US-743537.
(IDII-) IDI INFECTIO DIAC
BETGETO MG, QUEILETE M
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02-AUG-1984,

27-JAN-1984, U00144.

28-JAN-1983, GB-002349.

27-JAN-1984, GB-002211.

27-JAN-1984, GB-002186.
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Key
cds
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N40167 standard; DNA; 1212 BP.
N40167;
reptide epitope of sporozoite CS for vaccine to confer protection Disclosure, Fig 1, 67pp; English The inventors claim a peptide communication of a member of the genication o
                                                                                                                                                                                                  (UYNY-) NEW YORK UNIV.
Colman DR, Ellis J, Godson GN, Nussenzweig
VN, Schlesinger DH, Svec PS, Zavala F;
WPI; 84-201414/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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te M, Picard FJ,
peptide comprising an epport of the genus Plasmodium
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DNA encoding it (see N40167). The peptides may be used in vaccines to confer protection against malaria infections. The protective CS sporozoite antigens of Plasmodium possess a single immunodominant region composed of repetitions of the same epitope.

Sequence 1212 BP; 351 A; 287 C; 337 G; 237 T;

В

285 ttctcagaa 293

Matches Query Match Best Local

h 100.0%; Similarity 100.0%; 9; Conservative

Score 9; Pred. No. 0; Misma:

DB 3; Length 1212; 1.37e+03;

Mismatches

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1169 ttctcagaa 1177
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|33 ttctcagaa 25
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Clone #7A is a PCR product obtained from amplification of nucleic acids from serum samples of a Gulf War veteran (subject #1), diagnosed with Gulf War syndrome, using primers PGO2 and PGO3 (see V18154-55) that are based on poliovirus 5'-nontranslated and P2 regions. #7A is longer than the expected PCR product and shows no sequence identity to any known sequence (see also W18164-74). The invention provides hybridisation assays for the detection of target human nucleic acids in a biological sample. The methods are particularly useful for the early diagnosis of chronic illnesses such as cancer, multiple myeloma, autoimmune diseases, and neurodegenerative diseases (all claimed). The invention is also directed to the detection of non-poliovirus nucleic acids (e.g. directed to the detection of non-poliovirus nucleic acids (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-1998 (first entry)
Gulf War veteran subject #1 PCR clone #7A.
Picornavirus; poliovirus; enterovirus; vaccine; diagnosis;
chronic illness; polio; Gulf War syndrome; multiple myeloma;
prostate cancer; autoimmune disease; neuromuscular disease;
                                                                                                                                                                         syndrome patients and in patients diagnosed with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-1997; U17880.
04-OCT-1996; US-026762.
(CHRO-) CHRONIX BIOMEDICAL.
                                                                                                                                                                                           in vaccine polio preparations) and other viruses. Such recombinants h
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                                                                                                                         DNA encoding pancreas derived serpin - useful in diagnosis and treatment of pancreatic inflammation and disease Claim 2; Page 24; 36pp; English.

A cDNA clone (T42978), deisgnated Incyte 222689, codes for human pancreas-derived serpin (PDS) (W06202), a novel serine protease inhibitor. It was identified in a human pancreas library via phagemid cDNA clone isolation, sequencing and homology searching against a DNA sequence database. The cDNA can be used in the prodn. of recombinant PDS in host cells, and to design probes or primers useful in diagnostic tests for conditions associated with pancreatic inflammation. Antisense sequences can be used to treat pancreatic inflammation or disease.

Sequence 1221 BP; 417 A; 212 C; 249 G; 343 T;
                                                                            Query Match
Best Local
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02-MAY-1995; US-434881.
(INCY-) INCYTE PHARM INC
Braxton SM, Diep D, WI
WPI; 96-518311/51.
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W09634957-A1.
07-NOV-1996.
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Human pancreas derived serpin cDNA.
Pancreas derived serpin; PDS; serine protease inhibitor;
inflammation; antiinflammatory; diagnosis; gene therapy;
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Search completed: Thu Oct Job time: 198 secs. 28 00:33:22 1999

RESULT 200 ID T42978 standard; AC T42978;

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US-08-407-

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Sequence 11, Application Sequence 15, Application Sequence 15, Application Sequence 17, Application Sequence 17, Application Sequence 18, Application Sequence 19, Application Sequence 29, Application Sequence 21, Application 3, Sequence 22, Application 3, Sequence 23, Application 3, Sequence 24, Application 3, Sequence 25, Application 3, Sequence 26, Application 3, Sequence 27, Application 3, Sequence 28, Application 3, Sequence 29, 
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                                        APPLICANT:

APPLICANT:

TITLE OF INVENTION: CYTOKINES AND METHODS

NUMBER OF SEQUENCES: 165

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04477

FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/228,935

FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: SYNTHETIC DNA"
SEQUENCE 9 BP; 3 A; 2 C; 1 G; 3 T; 0 OTHER.
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US-08-385-
US-08-385-
US-08-180-
PCT-US94-0
US-08-736-
PCT-US96-0
US-08-736-
PCT-US96-0
US-08-758-1
US-08-768-1
US-08-7768-1
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            Score 9;
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                                                                                       NUCLEIC ACID
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            DB 4;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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LT 3
US-08-410-779B-35 STANDARD; DNA; UNC;
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                                                                                                SEQUENCE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-17025-34 STANDARD; DNA; UNC; 9
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TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17^^
FILING DATE: 28-DF0-1^^
CLASSIFT^^-
28-DF0-1^^
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                   1 TTCTCAGAA
                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JAN-
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF NUMBER OF SEQUENCES: 39
                                                                                                              HYPOTHETICAL:
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Curt A
APPLICANT: Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: James E. Darnell, Jr. APPLICANT: Zilong Wen
                                                                                                                     MOLECULE TYPE:
                                    ttctcagaa 25
                                                                                                                                                                                                   NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTCAGAA 9
                                                                                                                                                                                                                                                                                                                                  COUNTRY: CZIP: 07601
                                                                                                                             TOPOLOGY:
                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.0%;
9; Conservative
                                                                                                BP; 3 A; 2 C; 1
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                                                                                                                                           nucleic acid
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411 Hackensack Avenue
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                                                                                                                                                                                                                                                                                                                                          USA
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Curt M. Ho
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                                                                                                                                    double
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PC/TUS9517025
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                                                                  Score 9; DB 4; Le
Pred. No. 3.96e+02
0; Mismatches
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
DESCRIPTION: SYNTHETIC DNA"
SEQUENCE 9 BP; 3 A; 2 C; 1 G; 3 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/08410779B
Sequence 35, Application US/08410779B
Patent No. 5814517
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                                                                                                                                                                                                                                                                                       US-08-369-796-34 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 550-76:
TELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: JURGENSEN, THOMAS E
REGISTRATION NUMBER: 34,11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                       1 TTCTCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS ADDRESSEE: Klauber
                                               APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                           APPLICANT:
                                                                                                                                 APPLICANT: James E. D. APPLICANT: Zilong Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 550-7675
                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 016-0013A.US
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9393 TOWNE CENTRE DRIVE
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                                                                                                               Curt M. Horvath
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27-MAR-1995
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                                                                                                                                                     Darnell,
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Pred. No. 3.96e+02;
0; Mismatches 0;
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TO CYTOKINES AND METHODS FOR THEIR
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Klauber & Jackson

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TELEX: 13521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1 FNIGTH: 9 base pairs
                                                                                                                                                                                                               Patent No. 5712094
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SEIDEL, H. MARTI
APPLICANT: LAMB, I. PETER
APPLICANT: CHAN, SHIN-SHAY TIAN
APPLICANT: TININGTON AND
                                                                                                                                                                                                                                                                                                                 JT 5
US-08-411-020-13 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                       Sequence 13,
Sequence 13,
                                                                                                                                                                                                                                                                                                        XXXXXX
                 QOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,020
FILING DATE: 27-MAR-1995
CTARSTETCATUM. 478
                                                                                                                                                                                                                                                                                                                                                              33 ttctcagaa 25
                                                                                                                                                                        TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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QUENCE 9 BP; 3 A; 2 C; 1 G; 3 T; 0 OTHER
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                     STREET: 9393 Towne CITY: San Diego STATE: California COUNTRY: US
   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 TTCTCAGAA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
           FILING DATE: 2: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                           ZIP:
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Similarity 100.0%;
9; Conservative
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    Application US/08411020
    Application US/08411020
    5712094

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Hackensack
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Pred. No.
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3.96e+02;
                                                       Version #1
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Query Match
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DESCRIPTION: /desc = "OTHER NUCLEIC ACID.
DESCRIPTION: SYNTHETIC DNA"
SEQUENCE 9 BP; 3 A; 2 C; 1 G; 3 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXX
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                                                                                            REFERENCE/DOCKET NUMBER: 016-0013A.US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 550-7675
TELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (619) 557-7675
TELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 ttctcagaa 25
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                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MERAL INFORMATION:

APPLICANT: SEIDEL, H. MARTI

APPLICANT: LAMB, I. PETER

TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS

TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
 MOLECULE TYPE:
DESCRIPTION:
                                                                   SEQUENCE CHARACTERISTICS LENGTH: 19 base pairs
                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                           STRANDEDNESS: single TOPOLOGY: linear
                                                    LENGTH: 19 base pairs
TYPE: nucleic acid
                                                                                                                                                                 NAME: JURGENSEN, THOMAS E REGISTRATION NUMBER: 34,195
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/410,779B FILING DATE: 27-MAR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                  CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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 other nucleic acid
/desc = "OTHER NUCLEIC ACID,
                                                                                                                                                                                                                      US 08/228,935
                                                                                                                                                                                                                                                                                                      Release #1.0, Version
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US/08410779B
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Pred. No. 3.96e+
0; Mismatches
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3.96e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: SEQUENCE 19 BP; 6
                                                                                                   Sequence 57, Application US/08411020 Sequence 57, Application US/08411020 Patent No. 5712094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 101, Application Sequence 101, Application GENERAL INFORMATION:
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                                                                                                                                                  US-08-411-020-57 STANDARD; DNA; UNC;
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SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
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                       APPLICANT: LAMB, I. PETER
APPLICANT: CHAN, SHIN-SHAY TIAN
APPLICANT: CHAN, SHIN-SHAY TIAN
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACT
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                 APPLICANT:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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                 ADDRESSEE:
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Similarity 100.0%;
9; Conservative
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Similarity 100.0%;
9; Conservative
                                                                                           INFORMATION:
      E: Ligand Pharmaceuticals 9393 Towne Centre Drive
                                                                                 SEIDEL, H. MARTI
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A; 4 C; 5 G
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Floppy disk
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PC/TUS9504477
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Pred. No.
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3.96e+02;
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3.96e+02;
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                 Incorporated
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                                             CYTOKINE ACTION
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Query Match
Best Local
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/228,935
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 57
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
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DESCRIPTION: /desc = "OTHER NUCLEIC ACID.
DESCRIPTION: SYNTHETIC DNA"
SEQUENCE 19 BP; 6 A; 4 C; 5 G; 4 T; 0 OTHER.
   SEQUENCE 19 BP;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 100, Application PC/TUS9504477 Sequence 100, Application PC/TUS9504477 GENERAL INFORMATION:
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
DESCRIPTION: SYNTHETIC DNA"
QUENCE 19 BP; 4 A; 5 C; 4 G; 6 T; 0 OTHER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jurgensen, Thomas E.
REGISTRATION NUMBER: 34.195
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 550-7675
TELEPHONE: (619) 550-7675
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
                                                                           LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                            TOPOLOGY:
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Similarity 100.0%;
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Pred. No.
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local Similarity 100.0%;
Matches 9; Conservative
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DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
DESCRIPTION: SYNTHETIC DNA"
SEQUENCE 19 BP; 4 A; 5 C; 4 G; 6 T; 0 OTHER.
                                    US-08-411-020-56
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US-08-410-779B-100 STANDARD; DNA; UNC; 19
  Sequence
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APPLICANT: SEIDEL
APPLICANT: LAMB,
                                                                                                                                                                                                                                                                          TELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
                                                                                    33 ttctcagaa 25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,779B
FILING DATE: 27-WAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                8 ATTCTCAGAA 16
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08,
FILING DATE: 14-APR-1994
ATTORNEY_AGENT INFORMATION:
NAME: JURGENSEN, THOMAS E
REGISTRATION NUMBER: 34,15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 016-0013A.US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 550-7675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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STATE: CALIFORNI
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                     nucleic acid
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Application US/08411020
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                                    STANDARD; DNA; UNC;
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US/08410779B
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Pred. No. 3.96e+02
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No. 3.96e+02;
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DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
DESCRIPTION: SYNTHETIC DNA"
SEQUENCE 19 BP; 4 A; 5 C; 4 G; 6 T; 0 OTHER.
                                                                                                                                                                                                         JT 12
US-08-723-415B-21 STANDARD; DNA; UNC; 20
                                                                                                                                                                Sequence 21, Application Sequence 21, Application
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                                                                                                                                                        Patent No.
                                                                                                                        GENERAL INFORMATION:
APPLICANT: LaThangue,
APPLICANT: deLaluna,
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 535-390
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Releation DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                     8 TTCTCAGAA 16
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33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                            Local
STATE: V. STATE: V. COUNTRY: USA COUNTRY: 22201-4741
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jurgensen, Thomas E. REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 01f
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 550-7675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SEIDEL, H. MARTI
APPLICANT: LAMB, I. PETER
APPLICANT: CHAN, SHIN-SHAY TIAN
APPLICANT: CHAN, SHIN-SHAY TIAN
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
    COMPUTER READABLE FORM:
                                                                             CORRESPONDENCE ADDRESS:
                                                                                          NUMBER OF SEQUENCES:
                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                             CITY: Arlington
                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                     ADDRESSEE:
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9; Conservative
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California
                                                                                                                                                          5859199
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9393 Towne Centre Drive
                                                         1100 NO. 5859199th Glebe
                                                                                                                                                                                                                                                                                                                                                                                                                    19 base pairs
                                                                                                                                   LaThangue, Nicholas
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US/08723415B
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Pred. No.
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Best Local S
Matches
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEPAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application PC/TUS9410261A Sequence 20, Application PC/TUS9410261A GENERAL INFORMATION:
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Local Similarity 100.0%;
hes 9; Conservative
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                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: GB 9
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R
                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                APPLICANT: Gil, Susanna A. APPLICANT: Ryan, Maureen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTCTGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "PRIMER"
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LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Epiligrin, TITLE OF INVENTION: Integrins
                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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TYPE: n
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SOFTWARE: Patenti
                                                                                FILING DATE: 0
CLASSIFICATION:
                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: II
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                                                                                                       APPLICATION NUMBER:
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1420 Fifth Avenue
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 3.96e+
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application Sequence 18, Application
                                                                                                            APPLICATION NUMBER: US 08/537,874
FILLING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02126
FILLING DATE: 17-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: DUNN, TRACY J.
REGISTRATION NUMBER: 34,587
REGISTRATION NUMBER: 34,587
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, VC

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/564,955

FILING DATE: 30-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-564-955-18 STANDARD; DNA; UNC; 22
                                         TELEFAX: (415) 576-030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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MOLECULE TYPE:
DESCRIPTION:
HYPOTHETICAL: N
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                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/198,431
                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 17-FEB-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TTCTGAGAA
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ORGANISM: Hom
                                                                              REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: STEMMER, APPLICANT: CRAMERI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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            STRANDEDNESS:
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                    nucleic acid
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                                  22 base pairs
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METHODS FOR GENERATING POLYNUCLEOTIDES HAVING DESIRED CHARACTERISTICS BY ITER
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US/08564955
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Pred. No. 3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                           T 16
US-08-198-431-18 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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                                                                                                                                                                                  SEQUENCE
                XXXXX
                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                      FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 0180
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stemmer, Willem P.C.
APPLICANT: Crameri, Andreas
TITLE OF INVENTION: DNA Mutagenesis by Random FI
TITLE OF INVENTION: and Reassembly
MUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP PCT/US95/02126
FILING DATE: 17-FEB-1995
APPLICATION NUMBER: US 08/198,431
FILING DATE: 17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
                                                                                                                                                                                  TOPOLOGY: linear NCE 22 BP; 8 A; 4 C; 3
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                                                                                                                                            100.0%;
Similarity 100.0%;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                          Sequence 141, Application PC/TUS9300977
Sequence 141, Application PC/TUS9300977
Sequence 141, Application PC/TUS9300977
SEQUENCES: METHOD AND REAGENT NUMBER OF SEQUENCES: 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (oligonucleotide) SEQUENCE 22 BP; 8 A; 4 C; 3 G; 7 T; 0 OT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/198,431
FILING DATE: 17-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MOO1, Lesile
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 000324-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                        XXXXXX
                                                                                                                                                                                                                                                                                                      PCT-US93-00977-141 STANDARD; DNA; UNC; 26
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US93/0097'
FILING DATE: 19930129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Burns, Doane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stemmer, Willem P.C. TITLE OF INVENTION: Methods for NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1
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CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                       ttctgagaa 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                      COUNTRY: UP: 92660
                                                                                                                                                STATE:
     CLASSIFICATION:
                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                           Newport
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: 620 Newport Center Dr.
Newport Beach
CA
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Best Local :
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GENERAL INFORMATION:
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Sequence 663, Application US/08379078
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                                       TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
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Local Similarity 100.0%;
les 9; Conservative
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      TYPE: nucleic STRANDEDNESS: TOPOLOGY: line MOLECULE TYPE: C
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,078
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON
STREET: 620 Newport Center Drive
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Altman, Daniel E. REGISTRATION NUMBER: 34 - REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Gene Detection System NUMBER OF SEQUENCES: 726
                                                                                                                                                                                                                                                                                             APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                        REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                               CLASSIFICATION:
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TOPOLOGY: lir
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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Drive 16th Floor
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Query Match
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Best Local s
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Sequence 667, Application Sequence 667, Application Patent No. 5639612
GENERAL INFORMATION:
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SEQUENCE 26 BP;
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PCT-US93-00977-234 STANDARD; DNA; UNC; 26
                                                               XXXXX
                                                                             US-08-379-078-667 STANDARD; DNA; UNC; 26
                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US93/00977
FILING DATE: 19930129
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                                                                                                                                                                                             Local
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ANTI-SENSE: N
QUENCE 26 BP; 1
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                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Altman, Daniel E.
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ZIP: 92660
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REFERENCE/DOCKET NUMBER:
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Similarity 100.0%;
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BP; 10 A; 4 C;
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Dr. Sixteenth Floor
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Mitsuhashi, Masato

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US-08-379-078-553 STANDARD; DNA; UNC;
                                                                                                                                            Sequence 553, Application US/08379078 Sequence 553, Application US/08379078 Patent No. 5639612
                                                                                                                                                                                XXXXXX
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                    GENERAL INFORMATION:
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 714-760-940
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       33 ttctcagaa 25
                                                                                                                                                                                                                                                                Local Similarity 100.0%;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                        5 TTCTCAGAA 13
                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE: NO
DUENCE 26 BP; 10 A; 4 C; 6 G; 6 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/974,406
FILING DATE: 12-NOV-1992
                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
-STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:

NAME: Altman, Daniel E.

REGISTRATION NUMBER: 34,1

REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
TITLE OF It
                                                                                                     TITLE OF INVENTION: Gene Detection NUMBER OF SEQUENCES: 726
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 714-760-0404
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MEDIUM TYPE: Floppy disk
                                                                                                    NUMBER OF SEQUENCES:
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STATE:
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                                           COUNTRY: UZIP: 92660
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PR: HITACHI.011CP2
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TOPOLOGY: 11
                                    LENGTH:
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Sequence 181, Application PC/TUS9300977
Sequence 181, Application PC/TUS9300977
GENERAL INFORMATION:
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SEQUENCE 26 BP; 10 A; 4 C;
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PCT-US93-00977-181 STANDARD; DNA; UNC; 26
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APPLICATION NUMBER: US 07/974
FILING DATE: 12-NOV-1992
ATTORNEY_AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: HITA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-9404
TELEPAX: 714-760-9502
                                                                     TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                              REFERENCE/DOCKET NUMBER: HI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19930129
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA NUMBER OF SEQUENCES: 711
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TYPE: NUCLEIC ACID STRANDEDNESS: doub TOPOLOGY: linear
                                                                                         TELEPHONE: 714 / TELEPHONE: 714-760-9502
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CLASSIFICATION: 435
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Similarity 100.0%;
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    Knobbe, Martens, Olson, and Bear
620 Newport Center Dr. Sixteenth Floor
swport Beach

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Pred. No.
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3.96e+02;
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Best Local :
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Sequence 558, Application US/08379078 Sequence 558, Application US/08379078 Patent No. 5639612 GENERAL INFORMATION:
                                                        T 24
US-08-379-078-558 STANDARD;
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 176, Application PC/TUS9300977 Sequence 176, Application PC/TUS9300977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GÉNERAL INFORMATION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA NUMBER OF SEQUENCES: 711

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEPAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 176:
                                                                                                                                             y Match 100.0%;
Local Similarity 100.0%;
hes 9; Conservative
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Local Similarity 100.0%;
es 9; Conservative
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDN HYPOTHETICAL: NO
                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Altman, Daniel E.
                                                                                                                                                                                                                                                    TYPE: 1
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: POFILING DATE: 19930129 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                     ttctcagaa
                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006H
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ZIP: 92660
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CITY: Newport Beach
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26 BP; 10 A; 4 C;
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NUCLEIC ACID
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620 Newport Center
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Pred. No. 3.96e+02
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Dr. Sixteenth Floor
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3.96e+02;
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Matches
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Sequence 226, Application PC/TUS9300977
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT
NUMBER OF SEQUENCES: 711
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                                                                                                                                                                                                                                                                                                                                                                                                                            XXXXX
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PCT-US93-00977-226 STANDARD; DNA; UNC;
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NAME: Altman, Dante, 34,115

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: HITA

TELECOMMUNICATION INFORMATION:

THE TELECOMMUNICATION INFORMATION INFORM
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INFORMATION FOR SEQ
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Local Similarity 100.0%;
nes 9; Conservative
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HYPOTHETICAL: 1
ANTI-SENSE: NO
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                                                                                                 COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                        NUMBER OF ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
ADDRESSEE: Knobbe, Martens Dr. Sixteenth Floor
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ATTORNEY/AGENT INFORMATION:
Altman, Daniel E.
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APPLICATION NUMBER: US
FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Gene Detection System
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
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             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
URRENT APPLICATION DATA:
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TELEPAX: 714-760-9502
TELEFAX: 700 SEQ ID NO:
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STRANDEDNESS: doub
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APPLICATION NUMBER:
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26 BP; 10 A; 4 C;
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SEQUENCE 26 BP; 10 A; 4 C;
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US-08-431-527A-5 STANDARD; DNA; UNC;
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TELEFAX: 714-760-9502
INFORMATION, FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                          INFORMATION FOR SEQ ID NO:
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Local Similarity 100.0%;
nes 9; Conservative
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to
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MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
COPPUNDE: Word for windows version 3.10
                                                                        - REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-6938541
                                                                                                                                                                                                      SOFTWARE: Word for Windows version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           APPLICANT: David Segev TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                               SEQUENCE CHARACTERISTICS
                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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ANTI-SENSE: 1
                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                 STATE: Marvland
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                                                                                                       NAME: Friedmam, Mark M. REGISTRATION NUMBER: 33,883
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HI
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CLASSIFICATION:
TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                ZIP: 20906
                                                                                                                                                  APPLICATION NUMBER:
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                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                              972-3-6938542
                                                                                                                                                                                                                                                                                          United States of America
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Pred. No. 3.96e+02;
0; Mismatches (
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Best Local Similarity 100.0%;
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Best Local Similarity 100.0%;
                                                                                                                                                                                                  TELEPHONE: (617) 542-5070
TELEX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 38
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: SEQUENCE 27 BP;
                               T 28
PCT-US95-15716-37
                                                                                                                                                            MOLECULE TYPE: DNA
SEQUENCE 28 BP; 7 A; 7 C; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38, Application Sequence 38, Application GENERAL INFORMATION:
Sequence 37, Application PC/TUS9515716
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PCT-US95-15716-38 STANDARD; DNA; UNC; 28
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/348
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0613
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
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                                                                        33 ttctcagaa 25
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE Fish & Richardson
CORRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PCR AMPLI
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                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: 11n
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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VENTION: PCR AMPLIFICATION
VENTION: VARIABLE REGIONS C
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5 A; 9
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                                STANDARD;
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PC/TUS9515716
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Pred. No.
                                DNA; UNC;
                                                                                                                  Score 9; DB 4; L
Pred. No. 3.96e+02
0; Mismatches
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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PCT-US95-15716-23 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA SEQUENCE 28 BP; 8 A; 6 C; 6 G; 8 T; 0 OTHER
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           18 TTCTCAGAA 26
                                                                                                                                                                                                                                                                                 33 ttctcagaa
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                 APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
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STREET: ...
STREET: ...
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nucleic acid
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PC/TUS9515716
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Pred. No. 3.96e+02;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08431527A
Sequence 3, Application US/08431527A
Patent No. 5843550
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA SEQUENCE 28 BP; 8 A; 8 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-431-527A-3 STANDARD; DNA; UNC; 29
                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdis
COMPUTER: Twinhead Slimnote-890TX
COMPUTER: Twinhead Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,527A
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|33 ttctcagaa 25
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APPLICATION NUMBER: US 08,

FILING DATE: 01-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
Local Similarity 100.0%;
Nes 9; Conservation
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                         REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-6938541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1
MOLECULE TYPE:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                         ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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CITY: Silver Spring
                                                                                             FILING DATE:
                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Mark M. Friedman c/o Robert Sheinbeir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                      Maryland
                                                                                                                                                                                                                                                           United States of America
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Pred.
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DB 4; Le 3.96e+02; OTHER

Length 28;

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APPLICATION UNMER: US/08/117

FILING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190

REGISTRATION NUMBER: A-58

TELEPHONE: 415-781-1989

TELEPHONE: 415-781-1989

TELEPHONE: 415-781-1989

TELEPAX: 415-398-3249

TELEPAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
                                                                                   MOLECULE TYPE: cDNA SEQUENCE 31 BP; 7 A; 6 C; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51,
Sequence 51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXXXXX
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Local Similarity 100.0%;
hes 9; Conservative
                     17 TTCTGAGAA 25
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TTCTGAGAA 12
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                               LENGTH:
TYPE: n
                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                             STREET: 4 Embarcadero Center,
CITY: San Francisco
STATE: CA
ttctgagaa 33
                                                                                                           TOPOLOGY:
                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
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                                        h 100.0%;
Similarity 100.0%;
9; Conservative
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29 BP; 9 A; 5 C; 9
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Application US/08117083
                                                                                                           linear
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                                         Score 9; DB 2;
Pred. No. 3.96e+0;
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Pred. No. 3.96e+
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                                                      3.96e+02
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                                                               Length 31;
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Best Local s
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NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: NUMBER: 20-JAN-1995
LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application Sequence 11, Application GENERAL INFORMATION:
                                                                              Sequence 11, Application Sequence 11, Application Patent No. 5770717
                                                                                                                                                                                                                                                                                ANTI-SENSE:
SEQUENCE 32 BP;
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PCT-US96-00845-11 STANDARD; DNA; UNC; 32
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                                                                                                                                         US-08-376-157B-11 STANDARD; DNA; UNC; 32
                                                                    GENERAL INFORMATION:
                                                                                                                                                                                    33 ttctcagaa 25
APPLICANT: Golemis,
APPLICANT: Khazak, \( \)
APPLICANT: Estojak,
APPLICANT: Estojak,
TITLE OF INVENTION:
                                                                                                                                                                                                            18 TTCTCAGAA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Golemis, Erica A.
APPLICANT: Khazak, Vladimir
APPLICANT: Estojak, Joanne
TITLE OF INVENTION: Nucleic Acid Encoding a
TITLE OF INVENTION: Stress-Responsive Subunit
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                               Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/008-FILING DATE: 17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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CITY: Philadelphia
STATE: PA
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ZIP: 19103-2307
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            INVENTION: Nucleio
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1601 Market Street Suite 720
                                Fox Chase, Cancer Center
Golemis, Erica A.
Khazak, Vladimir
                                                                                                                                                                                                                                                                            NO 12 A; 4 C;
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 Nucleic Acid Encoding a Stress-Responsive Subunit of Human RNA Polymerase
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US/08376157B
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PC/TUS9600845
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Pred. No.
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No. 3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Sequence 20, Application US/08425684
Patent No. 5834252
GENERAL INFORMATION:
                                                                                                                                                                                                                                                          US-08-425-684-20 STANDARD; DNA; UNC; 40
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 32 BP; 12 A; 4 C; 8 G; 8 T; 0 OTHER.
                                                                                                                                                                                                                                                XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36.25
                                                                                                                                                                                                                                                                                                  33 ttctcagaa
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                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
                                                                                                                                                               APPLICANT: STEMMER PH.D., WILLEM P.C.
TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
NUMBER OF SEQUENCES: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 17-JAN-1996
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy
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TYPE: n
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STREET: 1601 Marke
CITY: Philadelphia
                                                                                           ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                              STREET: ONE MARKET PLAZA, CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
  CLASSIFICATION:
         APPLICATION NUMBER: US/08/425,684 FILING DATE: 18-APR-1995.
                                                                                                     COUNTRY:
                                                                                     94105
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1601 Market Street
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) 563-4044
- NO: 11:
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Pred. No.
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Suite 720
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. 3.96e+02;
                                         Version #1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/938,084
FILING DATE: 1920828
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 1652
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/07938084
Sequence 1, Application US/07938084
Patent No. 5464945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular SEQUENCE 40 BP; 11 A; 10 C;
                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-938-084-1 STANDARD; DNA; UNC; 40 BP.
                                                                                                TELEFAX: (510) 522-128
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
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Local Similarity 100.0%;
hes 9; Conservative
                                            MOLECULE
QUENCE 40
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ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                           REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reynolds,
APPLICANT: Walsh, P.
TITLE OF INVENTION: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: DUNN ESQ., TRACY J.
                                                                TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                 STREET: 340 P
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STRANDEDNESS: double
TOPOLOGY: circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                       NUCLEIC ACID
                                            TYPE: DNA
BP; 12 A; 7
100.0%;
llarity 100.0%;
Conservative
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                                                                            single
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ID NO: 1
                                            (genomic) 7 C; 7 G;
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                                                                                                                                                                                                                                                                                                                                                                                                         Quantitation of Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                          Rebecca L.
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Pred. No.
Score 9; DB 1; Le
Pred. No. 3.96e+02;
0; Mismatches (
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                      Length 40;
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Matches
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REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8669
FELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 522-1285
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
FOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 40 BP; 9 A; 10 C; 7 G; 14
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Sequence 3,
Patent No.
                                                         Sequence 30, Appl:
Sequence 30, Appl:
Patent No. 564848
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US-07-938-084-3 STANDARD; DNA; UNC; 40
                                                       Patent No.
                                                                                               T 37
US-08-375-241-30 STANDARD; DNA; UNC; 41
                                                                                        XXXXXX
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                                                 GENERAL INFORMATION:
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                                                                                                                                                              Match 100.0%;
Local Similarity 100.0%;
es 9; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,084
FILING DATE: 19920828
                                                                                                                                              9 TTCTCAGAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reynolds, Rebecca L.
APPLICANT: Walsh, P. Sean
ITITLE OF INVENTION: A Chemiluminescent Method for the
TITLE OF INVENTION: Quantitation of Human DNA
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
        APPLICANT: Parodos, Kyriaki
APPLICANT: McCarty, Janice
TITLE OF INVENTION: Nucleic Acid Probes
TITLE OF INVENTION: Shigella
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS:
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CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTCAGAA
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Application
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US/07938084
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US/08375241
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06617A
FILING DATE: 1920728
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/738,800
FILING DATE: 31-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application PC/TUS9206617A Sequence 30, Application PC/TUS9206617A GENERAL INFORMATION:
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PCT-US92-06617A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/738
FILING DATE: 31-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: GTRS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-661-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 TTCTGAGAA 28
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Local Similarity 100.0%;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375.24
FILING DATE:
CLASSTETT:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                             APPLICANT: McCarty, Janice
TITLE OF INVENTION: Nucleic Acid Probes for the Detection
TITLE OF INVENTION: Shigella
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Parodos, Kyriaki
APPLICANT: McCarty, Janice
                                                                                                                                                                                                                 STREET: 200 East
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60680
ATTORNEY/AGENT INFORMATION
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STREET: Two Milli
CITY: Lexington
STATE: Massachus
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: Illinois
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                                                                                                                                                                                                                                                                                       E: Amoco Corporation
200 East Randolph Drive, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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Pred. No. 3.96e+02
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                             Query Match 100.0%;
Best Local Similarity 100.0%;
                                                        TOPOLOGY: linear SEQUENCE 41 BP; 11 A; 8 C; 11 G; 11 T; 0
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Sequence 18, Applicat
GENERAL INFORMATION:
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PCT-US92-06617A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-856-4972
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                      TELEFAX: 312-856-4972 INFORMATION FOR SEQ ID NO:
   14 TTCTCAGAA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 ttctgagaa 33
                                                                                                                                    REFERENCE/DOCKET NUMBER: 33,595
REFERENCE/DOCKET NUMBER: GTR90-04 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-856-7180
TELEPHONE: 312-65-7180
                                                                                                                                                                                      FILING DATE: 19920728
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/738,800
FILING DATE: 31-JUL-1991
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19920728
                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic A
                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Parodos, APPLICANT: McCarty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Galloway, Norval B.
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: GT
TELECOMMUNICATION INFORMATION:
                                                                              STRANDEDNESS:
                                                                                    TYPE: NUCLEIC ACID
                                                                                                                                                                      NAME: Galloway, Norval REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 111
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                                                                                                                                                                                                                                                                                                                 60680
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NUCLEIC ACID
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             Application
Application
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                                                                              single
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PC/TUS9206617A
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No. 3.96e+02;
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                                                          Sequence 17, Application Sequence 17, Application Patent No. 5811238
                                                                                                          T 41
US-08-564-955-17
                                                                                                                                                                                                                                SEQUENCE 41 BP; 11 A; 8 C;
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                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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 APPLICANT: CRAMERI, I
                                                                                                                                                                                              Local Similarity 100.0%;
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ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: GTI
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 31-JUL-1991
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MCCarty, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                   ttctcagaa
                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                                                                                                                                                                                                                                    STRANDEDNESS: single
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CLASSIFICATION:
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                                       STEMMER,
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                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acid
Shigella
WILLEM P.C.
ANDREAS M.
METHODS FOR GENERATING POLYNUCLEOTIDES
HAVING DESIRED CHARACTERISTICS BY ITER
RECOMBINATION
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US/08564955
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                                                                                                            DNA;
                                                                                                                                                                                                                                 11 G; 11 T; 0 OTHER.
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RESULT
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Best Local Similarity 100.0%;
Matches 9; Conservative
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
                                                                                                                                                                                                                                                                      Sequence 17, Application Sequence 17, Application Patent No. 5830721
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US-08-537-874-17 STANDARD; DNA; UNC; 42 BP.
                                                                                                                                                                                                                                                                                                                                  XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/564,955
FILING DATE: 30-NOV-1995
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/198,431
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,874
FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                NUMBER OF SEQUENCES: 62
CGRRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                             APPLICANT: Stemmer, Willem P.C.
APPLICANT: Crameri, Andreas
TITLE OF INVENTION: DNA Mutagenesis by Random Fragmentation
TITLE OF INVENTION: and Reassembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/02126
FILING DATE: 17-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: DUNN, TRACY J.
NAME: DUNN, TRACY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: TWO EMBARCADERO C.
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                     STATE:
                                                                                                                  CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
NCE 42 BP; 14 A; 9 C;
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US/08537874
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Pred. No. :
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CENTER, 8TH FLOOR
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                  ATTORNEY/AGENT INFORMATION:
NAME: MOOL LESLIe
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEPAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE 42 BP; 14 A; 9 C; 7 G; 12 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08198431 Sequence 17, Application US/08198431 Patent No. 5605793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JT 43
US-08-198-431-17 STANDARD; DNA; UNC; 42
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APPLICATION NUMBER: US 08,
FILING DATE: 17-FEB-1994
ATTORNEY, AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/198,431 FILING DATE: 17-FEB-1994 CLASSIFICATION: 435 CLASSIFICATION: 435
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SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,874
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               STREET: 699 Prince
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      JICANT: Stemmer, Willem P.C.
JE OF INVENTION: Methods for In Vitro Recombination
                                                                                                                                                                                                                                                                                                                                    22313
                                                                                                                                                                                                                                                                                                                                                                                             699 Prince Street
                                         42 base pairs
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Pred. No. 3.96e+02;
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       JT 45
US-08-758-306-558 STANDARD; DNA; UNC;
                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-431-527A-1 STANDARD; DNA; UNC; 54
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33 ttctcagaa 25
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APPLICANT: David
                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: sin
TOPOLOGY: linear
MOLECULE TYPE: DNA
EQUENCE 42 BP; 14 A; 9
                                                 43 TTCTCAGAA 51
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                                         \mathfrak{s}
                                                                                Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                   REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-6938541
                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte,
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 5843650-enzymatic method for MUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
                                                                                                       IENGTH: 54
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
UENCE 54 BP; 14 A; 14 C; ]
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Friedmam, Mark M.
                                                                                                                                                                                                                                                                                     SOFTWARE: WORD for Win
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             COMPUTER: Twinhead Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Mindows version 3.11
SOFTWARE: Word for Windows version 2.0
                                         ttctcagaa
                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                              CITY: Silver Spring
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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A; 9 C; 7 G; 12 T; 0
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US/08431527A
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Pred. No.
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                                                                         Score Pred. 0; M
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                                                        Sequence 1036, Application Sequence 1036, Application Patent No. 5612215
                                                                                           XXXXXX
                                                                                                                                                                                                     SEQUENCE
                                                 GENERAL INFORMATION:
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                         APPLICANT:
                                  APPLICANT:
                  APPLICANT:
                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                    <u>ن</u>
 INVENTION:
Gustofson, John
Stinchcomb, Dan T.
VENTION: METHOD AND REAGENT FOR TREATMENT
                                  Pavco,
                       McSwiggen, James
                                         Draper,
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Sequence 558, Application US/08758306
Sequence 558, Application US/08758306
Patent No. 5807743
US-08-390-850-1036 STANDARD; DNA; UNC; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. |
SOFTWARE: FastSeq Version 1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/7/
FILING DATE: December 3, 19
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                     4 UUCUCAGAA 12
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: (67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                         TOPOLOGY: linear
NCE 54 BP; 17 A; 11 C;
                                                                                                                                                        Similarity
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                                                                                                                                       Conservative
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633 West Fifth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/08/758,306
December 3, 1996
                                                                                                                                                      100.0%;
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TREATMENT OF DISEASES
ASSOCIATED WITH
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Pred.
3; M
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 103
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/354,>24
APPLICATION NUMBER: 13, 1994
APPLICATION NUMBER: 08/152,487
APPLICATION NUMBER: 08/152,487
FILING DATE: No. 5612215ember 12, 1993
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                   Sequence 1036, Application US/08435634
Sequence 1036, Application US/08435634
Patent No. 5731295
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear SEQUENCE 54 BP; 18 A; 12 C;
                                                                                                                                                                                                                                                                              XXXXXX
                                                                                                                                                                                                                                                                                           US-08-435-634-1036 STANDARD; DNA; UNC;
                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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STREET: b33 mc..
STREET: Suite 4700
CITY: Los Angeles
CTATE: Callfornia
                                                                         APPLICANT: Gustofson, John
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: OF AFTHRITIC CONDITIONS
TITLE OF INVENTION: OF AFTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          4 UUCUCAGAA 12
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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STREET: 633 West fil
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071
                                                   E: Lyon & Lyon
633 West Fifth Street
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633 West Fifth Street
                                                                                                                                                                                          Draper,
                                                                                                                                                              McSwiggen, James
                                                                                                                                                                              Pavco, Pamela
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Pred. No. 3.96e+
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APPLICATION NUMBER: 08/152,487
APPLICATION NUMBER: 08/152,487
FILING DATE: No. 5731295ember 12, 1993
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WAIDLITG, RICHARD
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/TOCKET NUMBER: 211/084
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 1036:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: DUCHER: 34 base pairs
                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08592029
Sequence 6, Application US/08592029
Patent No. 5763196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 54 BP; 18 A; 12 C;
                                                                                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                                                                                                                                                                                                                                                                                                US-08-592-029-6 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                         Patent No.
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33 ttctcagaa 25
                                                                                                                                                                                                                                                                            GENERAL
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APPLICATION UMBER: US/C FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/5
FILING DATE: February 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 66.7%;
                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                       COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    TITLE OF INVENTION: ASSAYS USING TITLE OF INVENTION: ASSAYS USING USING TITLE OF INVENTION: FRAGMENTS OF UNMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Dis
MEDIUM TYPE: storage
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                        STREET: 755 PAGI
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER STREET: . 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90071
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                                                                                                                                                                                                                                                     KHANNA, PYARE
                                                                                                                                                                                                                                                                 POWELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FastSEQ Version
           PatentIn Release #1.0, Version #1.30
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February 17, 1995
NUMBER: 08/354,920
December 13, 1994
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                                                                                                                                                                                                                                                               MICHAEL J.
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Pred. No.
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                              TELEPHONE: (510) 814-2863
TELEFAX: (510) 522-1285
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/07938084
Sequence 9, Application US/07938084
Patent No. 5464945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear SEQUENCE 54 BP; 14 A; 14 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-938-084-9 STANDARD; DNA; UNC; 60
TYPE: NUCE STRANDEDNESS: SING TOPOLOGY: linear MOLECULE TYPE: DNA POUENCE 60 BP; 20 A; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TTCTCAGAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Local Similarity 100.0%;
                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/938,084 FILING DATE: 19920828 CLASSIFICATION: 435
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
NFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
                                                                                                                                     REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 860
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A Chemiluminescent Method for the TITLE OF INVENTION: Quantitation of Human DNA NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reynolds, Rebecca L. APPLICANT: Walsh, P. Sean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 07110-1199
                                                                                                                                                                                                                                                                                                                                           STREET: 340.1
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/O
FILING DATE: 26-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                       340 Kingsland Street
                  DNA (genomic)
A; 10 C; 11 G;
                                                   single
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Pred. No. 3.96e+02
0; Mismatches
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                 19 T; 0 OTHER
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          Query Match
                          DATE: March 24, 1995
RELEVANT RESIDUES IN:
SEQUENCE 63 BP; 18 A; 15 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application PC/TUS9603940 Sequence 15, Application PC/TUS9603940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US96-03940-15 STANDARD; DNA; UNC; 63 BP
                                                                                                                                                                                                                                                                 TELEFAX: (609) 520-3259
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
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Local Similarity 100.0%;
nes 9; Conservative
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                                                                                                         LIBRARY: CDNA
PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C.,
AUTHORS: Aral, Frohman, Michael A., Kraner, Susan D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TTCTCAGAA 17
                                                                                                                                                                   ORGANISM: Human
CELL LINE: HeLa
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                 ANTI-SENSE: no ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                         TELEPHONE: (609) 520-3214
                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                              JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                                                                                                                                                                               LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Princeton
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LICANT: Mandel, Gail, Chong, Jayhong, LE OF INVENTION: REST Protein and DNA
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                                                                              Sodium Channel Gene
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3, 1995
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Pred. No.
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Pred. No.
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3.96e+02;
 DB 4; Length 63; 3.96e+02;
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               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                  SEQUENCE 63 BP;
                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/982,744B
FILING DATE: 10-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4122598.8
FILING DATE: 08-UNL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP92/01523
FILING DATE: 06-UNL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07982744B Sequence 2, Application US/07982744B Patent No. 5591604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 51
US-07-982-744B-2 STANDARD; DNA; UNC;
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                                                                                                                                                                     TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: double st
TOPOLOGY: linear
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40 TTCTCAGAA 48
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                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS/DOS
SOFTWARE: Word Perfect, converted into ASC11-Codes
                                                                                                                                                                                   REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 18/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Recombination of INVENTION: E. coli
                                                                                  FEATURE:
NAME/KEY:
                                                . LOCATION: 2 .. 63
OTHER INFORMATION: /
OTHER INFORMATION: 1
UENCE 63 BP; 19 A; 15 C
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttctcagaa 25
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                                                                                                                                                                                                                                                                                                                                                                                  STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Little, Melvyn
                                                                                                  CDS
1 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breitling,
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                                                                                  CDS
                                                                                                                                    double stranded
                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Antibodies at the surface
                                                /product = "protein containing the epitope
for the tubulin monoclonal antibody YOL1/34
C; 18 G; 11 T; 0 OTHER.
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               Score 9; DB 1; Le
Pred. No. 3.96e+02;
0; Mismatches (
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                                Length 63;
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                Indels
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                US-07-982-743-9 STANDARD; DNA; UNC; 66 BP
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Matches
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Best Local
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LOCATION: 1..63
SEQUENCE 63 BP; 19 A; 15
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,743
FILING DATE: 10-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SYSTEM 1500 FOR THE PORT OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application Sequence 16, Application Patent No. 5849500
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US-07-982-743-16 STANDARD; DNA; UNC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
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                                                              40 TTCTCAGAA 48
                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..63
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
ttctcagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Svensson, Leonard R. REGISTRATION NUMBER: 3033C REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Birch, St. STREET: P.O. Box 747 CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                      h 100.0%;
Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
E: DNA
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                                                                                                                                                                                                                                                                                                                                                                                 /label= linker
/note= "alterna
l(c)"
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                                                                                                                             Pred.
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                                                                                                                                                                                           Score 9;
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                                                                                                                                                                 No. 3.96e+02;
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Best Local S
Matches
Patent No. 5200336.

Patent No. 5200336.

APPLICANT: KONG, HUIMIN:SCHILDKRAUT, IRA

APPLICANT: KONG, HUIMIN:SCHILDKRAUT, IRA

TITLE OF INVENTION: RESTRICTION ENDONUCLEASE OBTAINABLE FROM

BACILLUS COAGULANS AND A PROCESS FOR PRODUCING THE SAME

NUMBER OF SEQUENCES: 3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/547,787
                                                                                                                                                                        NAME/KEY:
LOCATION:
SEQUENCE 66 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
                                                                       XXXXXX
                                                                             5200336-2 STANDARD; DNA; UNC;
                                                               01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Breitl
                                                                                                                                                                                                                                                                                           TELEPHONE: 703-205-800
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 3030
REFERENCE/DOCKET NUMBER: 187:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
TELEFAX: 703-205-8050
                                                                                                                     19 TTCTCAGAA 27
                                                                                                                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                            33 ttctcagaa 25
                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
les 9; Conservative
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CURRENT APPLICATION DATA:
APPLICATION UNABER: US/07/982,743
FILING DATE: 10-MAY-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Svensson, Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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21 A;
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O. Box 747
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US/07982743
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/note= "tag-linker/scAb boundary in plasmid
(nucleotides 523 - 589), see Fig. 1"
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Sequence
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US-08-477-830-5 STANDARD; DNA; UNC;
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TELEFAX: (303) 793-3433 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatic
OPERATING SYSTEM: MS-I
SOFTWARE: WordPerfect
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                                                                                                                                                                                                                                 FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,99
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 10-JUNE PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 7-JUNE-19
                                                                                                        APPLICATION NUMBER: 08/4
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   FILING DATE: 21-DECEMBER-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                       TELEPHONE: (303) 793-3333
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                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HIGH AFFINITY HIV
TITLE OF INVENTION: NUCLEOCAPSID NUCLEIC ACID LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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D NO:2:
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/536,428 FILING DATE: 11-JUNE-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 21-DE
                                                                                                                                                                                                         APPLICATION NUMBER: 07/931, FILING DATE: 17-AUGUST-1992
                                                                   REFERENCE/DOCKET NUMBER:
                                                                                 NAME: Diane H. McCle
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Denver
STATE: Colors
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Similarity 100.0%;
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BP;
                                                                                               Diane H. McClearn
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Application US/08477830
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                                                                                                                                       08/477,172
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Pred. No.
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Best Local Similarity
Matches 6; Consei
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SEQUENCE 77 BP; 18 A; 22 C;
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                                                           FILING DATE: 7-JUNE-1995

FILING DATE: 7-JUNE-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION NUMBER: 07/536,428

APPLICATION NUMBER: 07/964,624

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA: 08/117,991

FILING DATE: 8-SEPTEMBER-1993

PRIOR APPLICATION NUMBER: 07/931,474

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION NUMBER: 08/361,795

APPLICATION NUMBER: 08/361,795

APPLICATION NUMBER: 08/361,795

FILING DATE: 11-DECEMBER-1994

PRIOR APPLICATION DATA: 08/361,795

FILING DATE: 19-MAY-1995

APPLICATION NUMBER: 08/361,795

FILING DATE: 19-MAY-1995

APPLICATION NUMBER: 08/477,172

FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: PATRICK ALI
APPLICANT: LARRY GOLD
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       REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-D
SOFTWARE: WORDERFECT CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                            FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HIGH AFFINITY TITLE OF INVENTION: NUCLEOCAPSID NUMBER OF SEQUENCES: 29
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TYPE: nucleic acid
STRANDEDNESS: sing
TODOLOGY: linear
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Application US/08477530
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llarity 66.7%;
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Pred. No. 3.96e+02;
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                            NEX 44-2
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SEQUENCE 77 BP; 18 A; 22 C;
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APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIC
TITLE OF INVENTION: NUC
APPLICATION NUMBER: 08/471
FILING DATE: 19-MAX-1995
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,96
REFERENCE/DOCKET NUMBER: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compation
OPERATING SYSTEM: MS-
SOFTWARE: Wordperfect
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Local Similarity 66.7%;
les 6; Conservation
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                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714
FILING DATE: 10-JUNE-1991
                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,4
FILING DATE: 17-AUGUST-1992
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
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                                                                                                PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
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                                                                                                              APPLICATION NUMBER: 08/361,79 FILING DATE: 21-DECEMBER-1994
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/964,624 FILING DATE: 21-OCTOBER-1992
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                                                                                                                                   08/361,795
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Pred. No. 3.96e+02;
3; Mismatches (
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 NEX 44-2
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TELECOMMUNICATION INFORMATION:

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TELEFAX: (303) 793-2433
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                     GORRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,430
FILING DATE: May 15, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/08/65,285
PRIOR APPLICATION DATA:
APPLICATION UMBER: US. 07/876,285
FILING DATE: May 11 29, 1992
APPLICATION NUMBER: US. 07/918,313
FILING DATE: July 21, 1992
APPLICATION NUMBER: US. 08/003,963
FILING DATE: JUNGBER: US. 08/003,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18,
Sequence 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-441-430-18 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XXXXXX
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                                                        TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 base pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mathew, Christopher George Porter
TITLE OF INVENTION: Fanconi Anemia Type C Gene
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Polley, Esq.
ADDRESSEE: Klarquist, Sparkman, Campbell, Leigh &
ADDRESSEE: Whinston, LLP
STREET: 1218.W. Salmon, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FAPPLICANT: SAPPLICANT: V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 100.0%;
Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Disk, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
    TOPOLOGY: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS SOFTWARE: WordPerfect 5.1/A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 121 S.W
CITY: Portland
STATE: Oregon
                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 97204
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Application US/08441430
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                       Linear .
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                                          Double stranded
      Genomic DNA
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3.96e+02;
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Best Local S
Matches
                                                        Query Match
Best Local :
                                            Matches
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,084
FILING DATE: 19920828
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 3669
TELECHOME: (510) 814-2863
TELEPHONE: (510) 814-2863
                                                                                                             TELEFAX: (510) 522-1285
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 80 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/07938084
Sequence 10, Application US/07938084
Patent No. 5464945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
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US-07-938-084-10 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
SEQUENCE 80 BP; 19 A; 15 C; 14 G; 31 T; 1 OTHER
                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                     Local
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                      9 TTCTCAGAA 17
                                                                                        MOLECULE TYPE: DNA (genomic)
QUENCE 80 BP; 24 A; 15 C; 16 G; 25 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: A Chemiluminescent Method TITLE OF INVENTION: Quantitation of Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reynolds, Rebecca L. APPLICANT: Walsh, P. Sean
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 340 K
CITY: Nutley
STATE: NJ
ttctcagaa
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                                            h 100.0%;
Similarity 100.0%;
9; Conservative
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Similarity 88.9%;
8; Conservative
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                                                         Score 9;
Pred. No.
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Pred. No. 3.96e+02
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                                                                  DB 1;
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RESULT 60
ID US-07-9
AC : xxxxxx

IT 60 US-07-938-084-11 STANDARD; DNA; UNC; 100 BP

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Best Local Similarity 100.0%;
Matches 9; Conservative
                                               GENERAL INFORMATION:
APPLICANT: Reynolds, Rebecca L.
APPLICANT: Walsh, P. Sean
TITLE OF INVENTION: A Chemiluminescent Method for the
TITLE OF INVENTION: Quantitation of Human DNA
NUMBER OF SEQUENCES: 20
CGRRESPONDENCE ADDRESS:
ADDRESSE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                            Sequence 4, Application US/07938084
Sequence 4, Application US/07938084
Patent No. 5464945
                                                                                                                                                                                    T 61
US-07-938-084-4 STANDARD; DNA; UNC; 130 BP
                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/07938084
Sequence 11, Application US/07938084
                                                                                                                                                                                XXXXXX
                                                                                                                                                                                                                                                                                                                                        TELEFAX: (510) 522-1285
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,084
FILING DATE: 19920818
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: e----
NAME: e----
                                                                                                                                                                                                                           33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                        TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: line
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                            9 TTCTCAGAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: A Chemiluminescent Method for the TITLE OF INVENTION: Quantitation of Human DNA NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 814-2863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reynolds, Rebecca L. APPLICANT: Walsh, P. Sean
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sias Ph.D., Stacey R. REGISTRATION NUMBER: 32,630 REFERENCE/DOCKET NUMBER: 8669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 07110-1199
                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                               ULE TYPE: DNA (genomic)
100 BP; 30 A; 18 C; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 Kingsland Street
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Pred. No. 3.95e+02;
0; Mismatches (
                                                                                                                                                                                                                                                                                                 G; 32 T; 0 OTHER
                                                                                                                                                                                                                                                                               Length 100;
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                             MOLECULE TYPE: DNA (genomic) SEQUENCE 130 BP; 37 A; 23 C; 30 G;
                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-I
SOFTWARE: PATENTIN Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938
FILING DATE: 19920828
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8669
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
33 ttctcagaa
                     9 TTCTCAGAA 17
 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
n Release #1.0, Version #1
                                                                                                                                                                                                                                                                                                                                                         32,630
EP:
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                                                                     Score 9; DB 1; Li
Pred. No. 3.96e+02;
0; Mismatches (
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                                                                                                                                               40 T; 0 OTHER
                                                                                                          Length 130;
                                                                         Indels
                                                                         0;
                                                                         Gaps
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ESULT 62

D US-07-938-084-6 STANDARD; DNA; UNC; 130 BP.

C xxxxxx

T Sequence 6, Application US/07938084

C Sequence 6, Application US/07938084

Sequence 6, Application US/07938084
Sequence 6, Application US/07938084
Patent No. 5464945
GENERAL INFORMATION:
APPLICANT: Reynolds, Rebecca L.
APPLICANT: Walsh, P. Sean
TITLE OF INVENTION: A Chemiluminescent Method for the
TITLE OF INVENTION: Quantitation of Human DNA
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.2!
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/938,084
FILING DATE: 19920828
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: S1AS Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8669
TELEPANE: (510) 814-2863
TELEPHONE: (510) 814-2863
TELEPHONE: (510) 824-2185
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single

linear

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RESULT
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Query Match 100.0%;
Best Local Similarity 100.0%;
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Best Local
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Sequence 12,
Patent No. 55
                            NAME/KEY: (
LOCATION: 1
SEQUENCE 132 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                       COMPUTER: 1BM COMPUTER: 1BM COMPUTER: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,943
TILING DATE: 17-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XXXXXX
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INFORMATION FOR SEQ ID NO:
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Local Similarity 100.0%;
hes 9; Conservative
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                                                                                        MOLECULE TYPE: NO ANTI-SENSE: NO
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APPLICANT: HIRATASU, KAZUNARI
APPLICANT: TSUCHIYA, MASAKAKU
TITLE OF INVENTION: METHOD FOR ASSAYING ACTIVITY OF
TITLE OF INVENTION: PROPHENCLOXIDASE ACTIVATING ENZYME AND APPLICATION
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 289513
                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: Q3
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-293-7060
                                                                                                                                                                                                                                APPLICATION NUMBER: 28951
FILING DATE: 18-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,4
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                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                   LENGTH:
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                                                                                                                                      nucleic acid
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Application
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                                                                                                                                                                                           202-293-7860
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                     1...132
; 46 A; 34 C; 21 G; 31 T; 0 OTHER.
                                      Coding Sequence
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2 A;
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26 C; 28
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US/08343943
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 Score 9;
Pred. No.
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Pred. No. 3.96e+02
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  DB 1; Length 132; 3.96e+02;
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RESULT
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CC SE
CC PE
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                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Sequence 16, Application US/07858124
Sequence 16, Application US/07858124
Patent No. 5427932
GENERAL INFORMATION:
                                                        JT 65
US-07-858-124-16 STANDARD;
                                                                                                                                                                       CLONE:
                                               XXXXX
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                              147 TTCTGAGAA 155
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                                                                                                                                                                                MOLECULE TYPE: CI
IMMEDIATE SOURCE:
LIBRARY: Bone N
CLONE: 132750
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                                                                                             25 ttctgagaa
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MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: PSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/700,575
APPLICATION NUMBER: US/08/700,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J
REGISTRATION NUMBER: 36749
REFERENCE/DOCKET NUMBER: 51
                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTGAGAA 89
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CITY: PALO ALTO
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8, Application US/08700575
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Bandman, Olga
Hawkins, Phillip R.
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                                                                                                                                                                      40 A; 29
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                                                         DNA;
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Pred. No.
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3.96e+02;
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                                                                                                                                                    Length 156;
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RESULT
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DT X6
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CC CC
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Best Local
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                       Sequence 43, 1
Sequence 43, 1
Patent No. 560
GENERAL INFO
                                                                      US-08-398-627-43 STANDARD; DNA; UNC;
                                                                                                                                                                   SEQUENCE 161 BP; 47 A; 22 C;
                                                              XXXXX
                                                                                                              140 TTCTCAGAA 148
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/858,124
FILING DATE: 1920326
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/683,441
FILING DATE: 09-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L
REGISTRATION NUMBER: 30863
REFERENCE/DOCKET NUMBER: 89-263-2
                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-543-4219 INFORMATION FOR SEQ ID NO:
                                                                                                     ü
                                                                                                                                                                                                      PUBLICATION INFORMATION:
AUTHORS: Willard and Waye
TITLE: "Hierarchial order in chromosome-specific
TITLE: human alpha satellite DNA"
JOURNAL: Trends in Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-777-9257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Repeat Sequence Chr
TITLE OF INVENTION: Nucleic Acid Probes
NUMBER OF SEQUENCES: 22
                APPLICANT:
                                                                                                                                                                                                                                                             MOLECULE TYPE: GENOMIC DNA --human alpha satellite
                                                                                                                                                                                                                                                     HYPOTHETICAL:
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CITY: SE
STATE: C
COUNTRY:
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                                                                                                                                                                           PAGES: 192-198
DATE: 1987
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                                                                                                                                           100.0%;
Similarity 100.0%;
                        INFORMATION:
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R P-
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                                     Application US/08398627
Application US/08398627
                                                                                                                                    Conservative
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Steuart Street Tower, 18th Fl., One Market
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plaza
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Gray, Joe W
Barry, Gerard F.
Kishore, Ganesh M.
Stark, David M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat Sequence Chromosome Specific
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                                                                                                                                           Score
Pred.
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                                                                                                                                    Mismatches
                                                                                                                                            NO ,
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                                                                                                                                             DB 1; Le
3.96e+02;
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                                                                                                                                                  Length 161;
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 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Sequence 43, Application US/08090523
Patent No. 5498830
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Stark, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
TELEPAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
SEQUENCE 171 BP; 48 A; 32 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-MAR-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,523
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539763
APPLICATION NUMBER: US 07/539763
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TTCTGAGAA 10
                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 700 Chesterfield Parkway No. 5608149th CITY: St. Louis
                                                             ADDRESSEE: Grace L. STREET: 700 Chesterfield
                                        STATE:
                                                       CITY: St. Louis
63198
                                      M1ssour1
                      USA
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                                                                                                                                                       Enhanced Starch Biosynthesis
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                                                                             Bonner, Monsanto Co. BB4F
field Parkway No. 5498830th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,963
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Pred. No.
0; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Le
3.96e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 171;
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Floppy disk

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 68
US-07-858-124-20 STANDARD; DNA; UNC; 171 BP
APPLICATION NUMBER: US/07/858,124
FILING DATE: 19920326
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/683,441
FILING DATE: 09-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXXX
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Local Similarity 100.0%;
es 9; Conservative
                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
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FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Weier, Heinz-Ulrich G
APPLICANT: Gray, Joe W
TITLE OF INVENTION: Repeat Sequence Chromosome Specific
TITLE OF INVENTION: Nucleic Acid Probes
NUMBER OF SEQUENCES: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
UENCE 171 BP; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Steuart Stree
STREET: Plaza
CITY: San Francisco
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                            94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 07/539763
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Pred. No.
0; Misma
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3.96e-
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Query Match
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US-07-858-124-22 STANDARD; DNA; UNC;
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                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDWBER: US 07/
FILING DATE: 09-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 base pairs
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HYPOTHETICAL: NO
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: D010266 #1 0
                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/858,124
FILING DATE: 19920326
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Repeat Sequence Chromosome TITLE OF INVENTION: Nucleic Acid Probes NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Weier, Heinz
APPLICANT: Gray, Joe W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
NAME: Lauder, Leona L
REGISTRATION NUMBER: 30863
REFERENCE/DOCKET NUMBER: 89
FELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                         COUNTRY:
ZIP: 941
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TITLE: "High-resolution Alu banding of human
TITLE: chromosomes with biotinylated Alu-PCR products:
TITLE: use for in situ hybridization mapping" (AbstractionNAL: Am. J. Hum. Genet
                                                                                                                                                                                                                                                                                                                                                                            STREET: Steuart Street Tower, STREET: Plaza
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STRANDEDNESS: sing
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US/07858124
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¤=R: 89-263-2
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Pred. No.
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Best Local Similarity 100.0%;
Matches 9; Conservative
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TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 171 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, App
Sequence 21, App
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US-08-151-477A-21 STANDARD; DNA; UNC;
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APPLICANT: Michae
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          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/151,477A
FILING DATE: NO. 5830644ember 12, 1
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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APPLICANT:
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: Baldini et al.
TITLE: "High-resolution Alu banding of human
TITLE: chromosomes with biotinylated Alu-PCR products:
TITLE: use for in situ hybridization mapping" (Abstraction National Am. J. Hum. Genet
VOLUME: 46 (Suppl.)
PAGES: A87
                                                                                                                                                                                                                                          APPLICANT: Homeyoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELEOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVIT
                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                             ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071
  APPLICATION NUMBER: 08/038,766
                                                                                                                                                                                                                                                                                                                                                                                                                       21, Application US/08151477A
21, Application US/08151477A
                                                                                                                                                                                                                                                                                                                                                Jerry W. Shay
Woodring E. Wright
Elizabeth Blackburn
                                                                                                                                                                                                                                                                                                                Calvin B. Harley
Scott L. Weinrich
                                                                                                                                                                                                                                                                                         Catherine Strahl
Michael J. McEachern
                                                                                                                                                                                                                                                                                                                                        Nam Woo Kim
                                                                                                                                                                                                                                                                                                                                                                                        Michael D. West
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Pred. No. 3.96e+02
0; Mismatches
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
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                                                                                                                                                                                                  COUNTRY: U.S.A.
2IP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" D1s
MEDIUM TYPE: storage
COMPUTER: IBM Compati
OPERATING SYSTEM: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 TTCTCAGAA 49
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33 ttctcagaa 25
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                 APPLICATION NUMBER: 07/882,43
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,76
FILING DATE: MARCH 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 100.0%;
Local Similarity 100.0%;
Local Similarity 100.0%;
local Similarity 100.0%;
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                         SOFTWARE: WORD Perfect 5.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: MAY 13, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: March 24, 1 ATTORNEY/AGENT INFORMATION:
                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR TITLE OF INVENTION: TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                       NAME: Warburg, Richard REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                   Los Angeles
: California
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                                                                                                                                                                                                                                                                                                                     3: Lyon & Lyon
633 West Fifth
                                                                                                                                                                                                                                                                                                                                                                                                   Elizabeth Blackburn
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Woodring E. Wright
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                                                                                                   08/038,766
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Pred. No.
0; Mismat
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Best Local
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Sequence 21,
Patent No. 56
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                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Michae
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 TTCTCAGAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 100.0%;
Local Similarity 100.0%;
nes 9; Conservative
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                                                                                                                       APPLICATION NUMBER: 08/0
FILING DATE: March 24, 1:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
                                                                                                                                                               COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,051B
FILING DATE: NO. 5645986ember 12,
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Dis
MEDIUM TYPE: storage
COMPUTER: IBM Compati
                              SEQUENCE CHARACTERISTICS:
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF TITLE OF INVENTION: CONDITIONS RELATED TO TELEOMERE TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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STREET:
CITY: Lo
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                                                            TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                      NAME: Warburg, Richard REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                TELEPHONE:
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          STRANDEDNESS:
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California
                    nucleic acid
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                                                                                                                                                                                                                                                                                                                                                               INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                            EE: Lyon & Lyon
633 West Fifth
Suite 4700
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Application US/08153051B
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Woodring E. Wright
Elizabeth Blackburn
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                                                                                 (213) 489-1600
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Pred. No.
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                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                    ANTI-SENSE: NO
SEQUENCE 197 BP; 61 A; 37 C; 43 G; 56 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/07858124 Sequence 17, Application US/07858124 Patent No. 5427932
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                     158 TTCTCAGAA 166
                                                                                                                                                                                                                                                                                                              ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/858,124
FILING DATE: 19920326
                                                                                                                                                            TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 base pairs
\mathfrak{Z}_{\mathbf{3}}
                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 ttctcagaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weier, Heinz-Ulrich G
APPLICANT: Gray, Joe W
TITLE OF INVENTION: Repeat Sequence Chromosome Specific
TITLE OF INVENTION: Nucleic Acid Probes
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 89
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0'
FILING DATE: 09-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                       LENGTH: 197 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
ttctcagaa
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Steua
STREET: Plaza
           TOPOLOGY:
                                                                                                                                                                                                                                      NAME: Lauder, Leona L
REGISTRATION NUMBER:
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Pred. No.
0; Misma
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3.96e+02;
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                                                               Length 197;
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TO US-07-858-124-18 STANDARD; DNA; UNC; 197 BP

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Query Match
Best Local S
Matches
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                                                                                                         Sequence 29, Application PC/TUS9502576 Sequence 29, Application PC/TUS9502576 GENERAL INFORMATION:
                                                                                                                                                                XXXXXX
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/858,124
FILING DATE: 19920326
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/683,441
FILING DATE: 09-APR-1991
                                                                                                                                                                                                                                                158 TTCTCAGAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lauder Leona L
REGISTRATION NUMBER: 30863
REFERENCE/DOCKET NUMBER: 89-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
                         TITLE OF INVENTION: NOV.
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & C.
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Local Similarity 100.0%;
es 9; Conservative
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE: NO
NIENCE 197 BP; 60 A; 35 C; 42 G; 60 T; 0 OTHER.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 197 base pairs
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CORRESPONDENCE ADDRESS:
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                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weier, Heinz-Ulrich G
APPLICANT: Gzay, Joe W
TITLE OF INVENTION: Repeat Sequence Chromosome Specific
TITLE OF INVENTION: Nucleic Acid Probes
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 Boston
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              60 State Street, suite 510
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US/07858124
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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REGISTRATION NUMBER: 36,207
REFERENCE, DOCKET NUMBER: BWI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPEAX: (617)227-75941
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..135
SEQUENCE 261 BP; 97 A;
                                                                                                                                                                                                                                                                                                     Patent No. 584000000:
                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08928613
Sequence 3, Application US/08928613
                                                                                                                                                                                                                                                                                                                                                                                                US-08-928-613-3 STANDARD; DNA; UNC;
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                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               APPLICANT: Diep, Dinh
APPLICANT: Braxton, Scott M.
APPLICANT: Delegeane, Angelo M.
TITLE OF INVENTION: A NOVEL HUMAN CYSTEINE PROTEASE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 524
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM:
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STATE: CA
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                                                       APPLICATION NUMBER:
                                                                                                                                                  ZIP: 94304
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7: USA
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                                                                                                                                                                  USA
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E: cDNA
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SYSTEM: PC-DOS/MS-DOS
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                                                       US/08/928,613
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Pred. No. 3.96e+02
0; Mismatches
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                                                                                  Version
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08406248 Sequence 5, Application US/08406248 Patent No. 5736318
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LIBRARY: 001098
SEQUENCE 267 BP; 75 A; 40
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GENERAL INFORMATION:
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                                                            TELEPHONE: 617-330-131
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO:
                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MCDANIels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: HAZ-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
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                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                           SEQUENCE CHARACTERISTICS:
LENGTH: 297 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner, Ph.D.,
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD AND KIT FOR TITLE OF INVENTION: TRANSFORMED CELLS NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE:
                                                                                                                                                                                                                                       STATE: MA
COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                      STREET:
CITY: B
                                                                                                                                           APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 436
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         STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                      Boston
                                                                                                                                                                                                                                                                                 200 State Street
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Jones, D. Le
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DNA (genomic)
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3.96e+02;
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Best Local :
   Matches
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                                                                                                PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FTSSCY, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPX: 200154
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1,
Sequence 1,
Patent No. 5
                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE 331 BP; 79 A; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 1..297
SEQUENCE 297 BP; 93 A;
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                                                                                                                                                                                                                        OPERATING SYSTEM: MS-DOS (Version 5 SOFTWARE: WOrdberfect (Version 5.1) CURRENT APPLICATION NATA: APPLICATION NUMBER: US/08/171,385 FILING DATE:
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NAME/KEY:
LOCATION:
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Local Similarity 100.0%;
es 9; Conservative
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55S
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: Fish & R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: HPV-16
IMMEDIATE SOURCE:
CLONE: E7
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ORGANISM: Hum
                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Mediators of Chronic Allograft TITLE OF INVENTION: Rejection
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mary E. APPLICANT: Ulrike
                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                              LENGTH:
h 100.0%;
Similarity 100.0%;
9; Conservative
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02110-2804
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5527884
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           Score 9;
Pred. No.
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Pred. No.
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            DB 1; L
3.96e+02
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                    Length 331;
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Best Local Similarity 100.0%;
Matches 9; Conservative
         Sequence 3, Application US/08917456
Sequence 3, Application US/08917456
Patent No. 5866368
                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 217..34
SEQUENCE 342 BP; 85 A;
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States
COUNTRY: United States
ZIP: 2333-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,720
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/070,455
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/070,455
FILING DATE: 09-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08470720
Sequence 1, Application US/08470720
Patent No. 5824798
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US-08-917-456-3
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  GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                      NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 003300-293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 342 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                              MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 09-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WIKSTROM, Olle
APPLICANT: TALLBERG, Annel1
TITLE OF INVENTION: GENETICALLY ENGINEERED MODIFICATION OF
TITLE OF INVENTION: POTATO TO FORM AMYLOPECTIN-TYPE STARCH
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttctgagaa
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STATE: Virginia
                                                                                                                                                                                                                                                                            STRANDEDNESS:
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STREET: George Mason Bldg.,
                                                                                                                                                                                                                                                                     TOPOLOGY:
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PERSSON, Per T
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                                                                     STANDARD;
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                                                                     DNA; UNC;
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g., Washington & Prince Sts
                                                                     363
                                                                                                                                                                                      Length 342;
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                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 363 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear SEQUENCE 363 BP; 139 A; 57 C
                                                                                                                                                                                                Patent No. 5861260
GENERAL INFORMATION:
                                                                                                                                                                                                            Sequence 11, Application Sequence 11, Application Patent No. 5861260
                                                                                                                                                                                                                                                           XXXXXX
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                                                                                                                                                                                                                                                                                                                                         194 TTCTGAGAA 202
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SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
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NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 215-994-2252
TELEFFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                               Watch 100.0%; Local Similarity 100.0%; Local Similarity 100.0%; nes 9; Conservative
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                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/917,456
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MEDIUM TYPE: Diskett
                                                                                                                              NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Greenwood APPLICANT: Gentry, 1 TITLE OF INVENTION: NUMBER OF SEQUENCES:
  SOFTWARE: FastSEQ Version CURRENT APPLICATION DATA:
                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                        APPLICANT:
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                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                      STREET: 225 1
CITY: Boston
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OPERATING SYSTEM:
                                                                      ZIP: 02110-2804
                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                    225 Franklin Street
                                                                                                                                                                DOXSEY, Stephen J.
VENTION: DIAGNOSTIC METHODS FOR SCREENING
VENTION: PATIENTS FOR SCLERODERMA
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US/08743200
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Length 363;

72 G; 95 T; 0

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Best Local
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                  ATTORNEY/AGENT INFORMATION:
NAME: J.G. MU1111ns
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 149-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence
LOCATION: 2...373
SEQUENCE 375 BP; 131 A; 83 C; 88 G; 73 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application Sequence 15, Application Patent No. 5552293 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-438-123-15 STANDARD; DNA; UNC; 464 BP
                                                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
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                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U:
FILING DATE:
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Local Similarity 100.0%;
es 9; Conservative
                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                     APPLICANT: Lindholm et al TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 375 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/743,200 FILING DATE: 05-NOV-1996 PRIOR APPLICATION DATA: ,APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe, Price, LeBlanc & Becker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Fasse, J. Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: DOS Text File
                                                                                                                                                                                                                                                                  STREET: Suite 300
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fasse, J. Peter REGISTRATION NUMBER:
                                                                                                                                                                                                                                                22314
Nucleic acid
                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                          Suite 300, 99 Canal Center Plaza
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US/08438123
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Pred. No.
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3.96e+02;
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RESULT
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PCT-US93-10443-6 STANDARD; DNA; UNC; 495

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Matches
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                   Query Match
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Sequence 4,
Patent No. 5
                                                                                           TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) SEQUENCE 492 BP; 128 A; 118 C; 77 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 464 BP; 98 A; 109 C; 130 G; 127 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
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           189 TTCTGAGAA 197
                                                                                                                                                                            TELEFAX: (312)456-7776
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 TTCTCAGAA 42
 25
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                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/009,261
FILING DATE: 19930122
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 492 base pairs
                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)456-8000
                                                                                                                                                                                                                                    CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fentress, Susan B.
REGISTRATION NUMBER: 31,327
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus and Chestnut
STREET: 100 S. Wacker Drive, Suite 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Specific DNA Primers and Meth
TITLE OF INVENTION: Same to Detect Eperythrozoon
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 S. W.
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
ttctgagaa
                                                                                                                             TYPE: NUCLEIC ACID
STRANDEDNESS: unkno
                                            h 100.0%;
Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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Application US/08009261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oberst, Richard D. Gwaltney, Sharon M. Hays, Michael P.
 3
                                                                                                                 unknown
                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Specific DNA Primers and Method to Use
                                                        Score 9;
Pred. No.
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Pred. No. 3.96e+02
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                                                Mismatches
                                                                                             169 T; 0 OTHER
                                                           DB 1;
3.96e
                                                                   Length 492;
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                            GENERAL INFORMATION:
APPLICANT: David D. Moore
APPLICANT: Jae Woon Lee
TITLE OF INVENTION: NUCLEAR HORM
TITLE OF INVENTION: RELATED MOLE
TITLE OF INVENTION: RELATED MOLE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR. APPLICATION DATA:
APPLICATION NUMBER: 07/969,136
ETLING DATE: OCTOBER 30, 1992
ATTORNEY,AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 00786/09
REFERENCE,DOCKET NUMBER: 00786/09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application PC/TUS9310443 Sequence 6, Application PC/TUS9310443 GENERAL INFORMATION:
                                                                                                                                                       Sequence 6, Application US/08222719
Sequence 6, Application US/08222719
Patent No. 5846711
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear SEQUENCE 495 BP; 152 A; 130 C; 98 G; 114 T; 1 OTHER
                                                                                                                                                                                                            T 85
US-08-222-719-6 STANDARD; DNA; UNC; 495 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10443
                                                                                                                                                                                                                                                                                        410 TTCTCAGAA 418
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ADDRESSEE: Fish & Richardson
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APPLICANT: Jae W. Lee
TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
TITLE OF INVENTION: INVERACTING POLYPEPTIDES AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                STREET: 225 F
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: doub
 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
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 Massachusetts: U.S.A.
                                  225 Franklin Street
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                                                                     RELATED MOLECULES AND METHODS
                                                                                          NUCLEAR HORMONE RECEPTOR-
INTERACTING POLYPEPTIDES AND
                                                                                                                                                                                                                                                                                                                          Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                0,
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Best Local Similarity 100.0%;
Matches 9; Conservative
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REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 495
TYPE: 1954
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: David D.
APPLICANT: Jae Woon
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                            COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,925
FILING DATE: 06-June-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application Sequence 6, Application Patent No. 5866686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear SEQUENCE 495 BP; 152 A; 130 C; 98 G; 114 T; 1 OTHER
                                                                                                                                                                                                                                                                                                                                                                                    XXXXX
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FILING DATE: 04-April-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,136
FILING DATE: 30-October-1992
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Dis
COMPUTER: IBM PS/2 MO
OPERATING SYSTEM: MS-
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     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,719
FILING DATE: 04-April-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                    CITY: Boston
STATE: Massa
                                                                                                                                                                                                          STREET:
LASSIFICATION:
                                                                                                                                                                                   Massachusetts
                                                                                                                                                                                                           225 Franklin Street
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                                                                                                                                                                                                                                                                                                 Jae Woon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PS/2 Model 50z or 5: SYSTEM: MS-DOS (Version
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US/08470925
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INTERACTING POLYPEPTIDES AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US92-11353-13 STANDARD; DNA; UNC; 521 BP.
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,284
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PAIMElee, Steve W
REGISTRATION NUMBER: 31-990
REFERENCE/DOCKET NUMBER: 13952-13-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 542-89
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                      TELEFAX: 206-623-6793
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 TTCTCAGAA 418
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Local Similarity 100.0%;
                                                                                                                                                                                                REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEFAX: 01154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Grant, Francis J
APPLICANT: Sheppard, Paul O
TITLE OF INVENTION: NOVEL HUMAN TRANSGLUTAMINASES
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                         CITY: SE
STATE: C
COUNTRY:
      TYPE: NUCLEAR STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: Octobe CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: doubl
                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                San Francisco
                           NUCLEIC ACID
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                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                   19921230
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r 30, 1992
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Pred. No.
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                       CLONE: PTG562
SEQUENCE 521 BP; 136 A; 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T: 88
US-07-998-973A-13 STANDARD; DNA; UNC; 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: PTG562
SEQUENCE 521 BP; 136 A; 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application Sequence 13, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXXXX
                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 TTCTCAGAA 357
                      349 TTCTCAGAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atent No. 5514579
GENERAL INFORMATION:
                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 ttctcagaa 25
                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,284
APPLICATION NUMBER: 31-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sheppard, Paul O
TITLE OF INVENTION: NOVEL HUMAN TRANSGLUTAMINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steve W
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 521 base pairs
                                                                                                                                                                              TELEPHONE: 200 - TELEPHONE: 200 - TELEPHONE: 206-623-6793
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: One Market CITY: San Francisco
                                                                                                                                           TYPE: NUCLEIC ACID
                                                                                                                          TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: 19921230
                                                                                                                                                                                                                                     NAME: Parmelee, Steve W REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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Sheppard, Paul O
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                                                                                                                           linear
                                                                                                                                                                                                      206-467-9600
                                                                                                                                   single
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US/07998973A
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                                                                                                                                                                                                                                                                                                                            US/07/998,973A
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                                                       Score 9;
Pred. No.
                                                                                        C; 155 G;
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                                                       DB 1; Le
3.96e+02;
                                                                                         105 T; 0 OTHER
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                                                                 Length 521;
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RESULT
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US-08-171-385-4 STANDARD; DNA; UNC; 651

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Query Match
Best Local :
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Sequence 16, Application US/08322742
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Sequence 4, Application US/08171385
                                                                                                                                                                                                                                   US-08-322-742-16 STANDARD; DNA; UNC; 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5527884 GENERAL INFORMATION:
                                                                                                                                                  Patent No. 5688641
GENERAL INFORMATION:
                                                                                                                                                                                                                      XXXXXX
                                                                                                                                                                                                                                                                                        387 TTCTCAGAA 395
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| 33 ttctcagaa 25
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TELECOMMUNICATION INFORMATION: (617) 542-5070
TELEPAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/171,385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mary E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                               TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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STATE: Massachus
COUNTRY: U.S.A.
ZIP: 02110-2804
                                      STREET:
CITY: E
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: double
TOPOLOGY: linear
ENCE 651 BP; 218 A; 135 C; 168 G; 130 T; 0 OTHER.
            COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
STREET: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                              h 100.0%;
Similarity 100.0%;
9; Conservative
                                                   Boston
                                     Massachusetts
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                                                                  225 Franklin Street
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Pred. No.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 1
FILING DATE: 05-MOV-1993
PRIOR APPLICATION DATA:
                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                              COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: February 28, APPLICATION NUMBER: 07/552 FILING DATE: February 28, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Vaccinal Polypeptides NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                         STREET: U.S. Mailcode CITY: King of Prussia STATE: Pennsylvania
                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                  ADDRESSEE: SmithKl
ADDRESSEE: Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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COMPUTER: II
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Dillon, or
Tames
Va/
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nber 1, 1992
07/844,296
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07/552,216
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Pred. No.
0; Misma
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Sequence 1, Application PC/TUS9401149
GENERAL INFORMATION:
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PCT-US94-01149-1 STANDARD; DNA; UNC; 666
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SEQUENCE 666 BP; 224 A; 118
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                   33
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Local Similarity 100.0%;
nes 9; Conservative
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APPLICATION NUMBER: US 1
FILING DATE: 18-AUG-1993
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         TITLE OF INVENTION: Vaccinal Polypeptides NUMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 2
FILING DATE: 02-NOV-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Baumeister, Kirk REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 28-JU
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                                                                                                                                               ADDRESSEE: SmithKline Beecham Corporation - Corporate ADDRESSEE: Patents
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LOCATION: 1..
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TOPOLOGY: unl
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                                                                               COUNTRY:
                                                                                                                              STREET:
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                                                                                             King of Prussia
Pennsylvania
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                                                                                                                              U.S. Mailcode UW2220 - 709 Swedeland Road
                                                                                                                                                                                                                          Dillon, Susan B.
Kane, James
                                                                                 USA
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Scott, Miller
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1..663
SEQUENCE 666 BP; 223 A; 117 C; 167 G; 159 T; 0 OTHER
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PCT-US94-01149-7 STANDARD; DNA; UNC;
                                                                                                                                                                                                            XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5096
                                                                                                                                                                                                                                                                                                                         208 TTCTCAGAA 216
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 656 base pairs
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                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 645,732
FILING DATE: 30-AUG-1984
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 387,200
APPLICATION DATA:
APPLICATION NUMBER
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APPLICATION NUMBER:
FILING DATE: 30-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/01149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 18-FEB-
                                    CORRESPONDENCE ADDRESS
                                                TITLE OF INVENTION: Vaccinal Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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Scott, Miller
Dillon, Susan B.
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   SmithKline Beecham Corporation - Corporate Patents
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18-AUG-1993
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01-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double
                                                                               James
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Pred. No. 3.96e+02
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Best Local S
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Sequence 9, Application Sequence 9, Application Patent No. 5821070
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                                                        US-08-139-937-9 STANDARD; DNA; UNC;
                                                                                                                                                                                                LOCATION: 1..670
SEQUENCE 670 BP; 223 A; 117
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 837,773
APPLICATION DATA: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 751,896
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 387,200
FILING DATE: 28-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 238,801
FILING DATE: 02-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 645,732
APPLICATION NUMBER: US 645,732
APPLICATION NUMBER: US 645,732
APPLICATION INFORMATION:
NAME: BANDESTEET, X1*K
                                                                                                                             208 TTCTCAGAA 216
                                                                                                                                                                                                                                                                                                               TELEFAX: 215-270-5090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                             y Match 100.0%;
Local Similarity 100.0%;
                                                                                                    APPLICATION NUMBER: US 013,415
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 108,914
FILING DATE: 18-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 1-
FILING DATE: 05-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 670 base pairs
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5096
                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1..(
                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .: U.S. Mailcode UW2220 - 709 Swedeland Road
King of Prussia
                                                                                                                                                                                                                                                                             nucleic acid
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            US/08139937
US/08139937
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Pred. No.
0; Misma
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APPLICANT: BOARD OF REGENTS OF THE
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                    XXXXX
                                                                                                                                                                                                                                              PCT-US93-11310-9 STANDARD; DNA; UNC; 688
                                                                                                                                                                                                                                                                                             33 ttctcagaa
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                           CITY: :
                                                           COUNTRY: U
                                                                                 STATE:
                                                                                                                  ADDRESSEE:
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                                                                                          T: 4370 LA JOLLA
SAN DIEGO
                                                                                 CALIFORNIA
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                                                                      USA
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CAMPBELL AND FLORES
70 LA JOLLA VILLAGE DRIVE

BP.

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/139
FILING DATE: 20 OCT 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US 07/979
FILING DATE: 20 NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ
TELECOMMUNICATION INFORMATION:
TELEPAN: 619-535-9001
TELEFAN: 619-535-9001
TELEFAN: 619-535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
            292 TTCTCAGAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LEE, WEN-HWA
APPLICANT: SHAW, BEI
APPLICANT: SHAW, BEI
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                           MOLECULE TYPE: cDNA
NUENCE 688 BP; 253 A; 116 C; 149 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
                                                                                                                 STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                      nucleic acid
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                                           Score 9;
Pred. No.
0; Misma
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                                             Mismatches
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3.96e+02;
                                                                                             170 T; 0 OTHER.
                                                                    Length 688;
                                              Indels
                                             0;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9603940 Sequence 2, Application PC/TUS9603940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US96-03940-2 STANDARD; DNA; UNC; 756 BP
                                                                             TELEFAX: (609) 520-3259
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 TTCTCAGAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 ttctcagaa 25
                                                                                                                             NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                             SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 619-535-9001
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ATTORNEY/AGENT INFORMATION:
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ORIGINAL SOURCE:
ORGANISM: Hum
                            MOLECULE TYPE: cl
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                 STREET: P.O. DO. CITY: Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: FP-CJ
                                                                                                                      TELEPHONE:
                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: March
                                                                                                                                                                                                                                 COMPUTER: IBM-com
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                           New Jersey
                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                       Mandel, Gail, Chong, Jayhong A. VENTION: REST Protein and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619-535-8949
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                                                                                                                      (609) 520-3214
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                                                                                                                                                                                           March 23, 1995
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08216233C Sequence 1, Application US/08216233C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-216-233C-1 STANDARD; DNA; UNC; 776 BP
                                                          TELEPHONE: (305) 222-6423
TELEFAX: (305) 222-6666
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 776 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 TTCTCAGAA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Local Similarity 100.0%;
hes 9; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: cDNA
PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C.
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D.
TITLE: REST: A Mammalian Silencer Protein that Restricts
                                                                                                             REGISTRATION NUMBER: 34,745
REFERENCE/DOCKET NUMBER: BA-4203
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (305) 222-6423
                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 10-DEC-1991 ATTORNEY/AGENT INFORMATION: NAME: TYMESON, CYNTHIA G
                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
MOLECULE TYPE: DNA (genomic)
PUENCE 776 BP; 260 A; 138 C; 170 G; 208 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                          TOPOLOGY:
                                  STRANDEDNESS:
                                                TYPE: nucleic acid
                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 22-MA
                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     CITY: DEERFIELD
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1717 DEERFIELD ROAD
                                                                                                                                                                                                                                                                                                                                              USA
                          unknown
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                                                                                                                                                                                                                                    22-MAR-1994
                                      unknown
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Pred. No.
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"Indended Boutros, Michael C.,
"raner, Susan D.,
"raner, Susan D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; DB 4; Length 756; No. 3.96e+02;
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180 T; 0 OTHER.
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Mandel, Gail
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Query Match Best Local Matches

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Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative
            Sequence 5, Application US/08565386
Sequence 5, Application US/08565386
Patent No. 5741697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08117083
Sequence 7, Application US/08117083
Patent No. 5719054
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US-08-117-083-7 STANDARD; DNA; UNC; 790
                                                                                                                                                                                                                                     SEQUENCE 790 BP;
                                                                              US-08-565-386-5
                                                                                                                               766 TTCTCAGAA 774
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| 33 ttctcagaa 25
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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    GENERAL INFORMATION:
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                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
DUENCE 790 BP; 262 A; 143 C; 175 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                               NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: S
STATE:
                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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Similarity 100.0%;
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4 Embarcadero Center, Suite 3400
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Inglis, Stephen C.
Munro, Alan J.
                                                                              STANDARD;
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                                                                              DNA; UNC;
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Pred.
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Pred. No. 3.96e+02
0; Mismatches
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d. No. 3.96e+
Mismatches
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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SEQUENCE 792 BP; 226 A; 133 C; 1
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US-08-565-386-5 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                 Sequence 5, Patent No. 5
                                                                                                                                                                                                                                                                                                                                        Sequence 5,
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APPLICANT: Bavoil, Patrik M.
APPLICANT: Hsia, Ru-ching
                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 TTCTGAGAA 344
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NAME: Timian, Susan J.
REGISTRATION UNMER: 34,103
REFERENCE/DOCKET NUMBER: 176,
TELEPHONE: 716-263-1636
TELEPAX: 716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 716-263-1600 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 25 ttctgagaa 33
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LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                    SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 TITLE OF INVENTION: BACTÉRIOPHAGE NUMBER OF SEQUENCES: 23
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NUMBER OF SEQUENCES:
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NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 17
FELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
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STREET: Cl
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                                                                                                         APPLICATION NUMBER:
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, Application US/08565386
5741697
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Hsia, Ru-ching
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quare, P.O.
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quare, P.O. Box 1051
                                                                                                                                Release #1.0,
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Pred. No.
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                             176/60040
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Best Local S
Matches
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US-08-967-101-119 STANDARD; DNA; UNC; 796
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/592,541
APPLICATION NUMBER: 08/592,541
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
                                           450
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 119:
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Local Similarity 100.0%;
les 9; Conservative
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                                                                                                        Match 100.0%;
Local Similarity 100.0%;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA
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CORRESPONDENCE ADDRESS:
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COUNTRY:
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|ttctcagaa 25
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796 BP; 198 A; 134 C; 264
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19, Application
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High Street Tower - 125 High :
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ROMMENS, JOHANNA M
FRASER, PAUL E
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Pred. No.
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Pred. No. 3.96e+02
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                LENGTH: 796 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE 796 BP; 246 A; 165 C; 187 G; 198 T; 0 OTHER.
                                                                                                                                                    T 103
US-08-375-241-2 STANDARD; DNA; UNC;
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                                                                                                             Sequence 2, Application Sequence 2, Application
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PCT-US92-06617A-2 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06617A
FILING DATE: 19920728
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/738,800
FILING DATE: 31-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, NOTVal B.
REGISTRATION NUMBER: 33,595
                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312-856-4972
INFORMATION FOR SEQ ID NO:
                                                APPLICANT: Parodos, I
APPLICANT: McCarty,
TITLE OF INVENTION: I
TITLE OF INVENTION:
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LENGTH: 796 base pairs
TYPE: NUCLEIC ACID
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-856-7180
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                             CORRESPONDENCE ADDRESS:
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                                       NUMBER OF SEQUENCES:
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CITY: Chicago
STATE: Illinois
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                            Nucleic Acid
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                  Brook,
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                    Smith & Reynolds,
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                                                                                                                                                                                                                                                   Sequence 1, Application US/08407544
Sequence 1, Application US/08407544
Patent No. 5741657
                                                                                                                                                                                                                                                                                                T 104
US-08-407-544-1 STANDARD; DNA; UNC; 798
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 796 BP; 246 A; 165 C; 187 G;
                                                                                                                                                                                                                                                                                        XXXXXX
                                                                                                                                                                       APPLICANT: Tsien, Roger Y.
APPLICANT: Zlokarník, Gregor
TITLE OF INVENTION: FLUOROGENIC SUBST
TITLE OF INVENTION: BETA-LACTAMASE AN
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/407
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Spitals, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 1279
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 31-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 796 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                              33 TTCTCAGAA 41
                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%;
Local Similarity 100.0%;
les 9; Conservative
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: US
                                                                                                                            STREET: 210 N. Fig
CITY: Los Angeles
STATE: CA
COUNTRY: USA
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Y: U.S.A.
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                                                                       Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/375,241
                                                      US/08/407,544
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Pred. No. 3.96e+
0; Mismatches
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 1279-197
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3.96e+02;
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Best Local Similarity 100.0%;
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TELEPAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 798 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                            MOLECULE TYPE:
SEQUENCE 819 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 118, Application Sequence 118, Application Patent No. 5840540 GENERAL INFORMATION:
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LOCATION: 7..795
SEQUENCE 798 BP; 217 A; 185
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US-08-967-101-118 STANDARD; DNA; UNC; 819
                                                                                                                                                  NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 118:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 TTCTCAGAA 230
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Local Similarity 100.0%;
les 9; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
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STREET: High
CITY: Boston
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COUNTRY:
                                                                         STRANDEDNESS: S1
TOPOLOGY: linear
                                                                                                                                                                                                                                                             APPLICATION DATA:
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                                                                                                      nucleic acid
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High Street Tower - 125 High Street
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                                            : DNA (genomic)
185 A; 232 C; 1
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MENS, JOHANNA M
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977-1003
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US/08967101
   Score 9;
Pred. No.
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Pred. No.
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                                               162 G;
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3.96e+02
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 DB 3; Length 819; 3.96e+02;
                                               208 T;
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US-08-247-809A-11 STANDARD; DNA; UNC; 850 BP.
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                                                                                                                                                      SEQUENCE 850 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 TTCTGAGAA 435
                                                                                                                                       TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: genomic DNA
MOLECULE TYPE: 351 A; 83 C; 12
                                                                                                                                                                                                                              TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                            337 TTCTGAGAA 345
                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: WHITE JR., PAULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 ttctgagaa 33
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APPLICATION NUMBER: US/08/485,284.
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 43361/1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0/
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REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL VECTOR HAVING PROMOTER THAT IS TITLE OF INVENTION: INDUCIBLE BY METHANOL AND/OR GLYCEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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Similarity 100.08;
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SHIBANO, IU.
SHIBANO, IU.
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SHIBANO, IU.
SHIBANO, IU.
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                                                                                                                                                                                                                                                                                (202)
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                                                                                                     Sequence 15, Application Sequence 15, Application
                                                                                                                                                   .T 108
US-08-346-333-15 STANDARD; DNA; UNC; 858 BP
                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                          Patent No.
                                                                                                                                           XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Rurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bay
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: May 23, 1994
CLASSIFICATION: 800
PROOR APPLICATION DATA:
APPLICATION NUMBER: P 43.1
FILING DATE: May 28, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                        25 ttctgagaa
 APPLICANT: Botstein, David
APPLICANT: Palzkill, Tinmothy
TITLE OF INVENTION: Methods for modifying DNA and for
TITLE OF INVENTION: detecting effects of such modification on
TITLE OF INVENTION: encoded modified polypeptides with target
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10591-5144

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0

MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 2..799
LOCATION: 291 A; 145
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OPERATING SYSTEM: DOS
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Similarity 100.0%;
9; Conservative
                                                                               INFORMATION:
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Application
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US/08247809A
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RESULT ID US

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 858 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1.858
SEQUENCE 858 BP; 221 A; 205 C; 220 G; 212 T; 0 OTHER
                                                                                                                                                 Sequence 15, Application PC/TUS9107506 Sequence 15, Application PC/TUS9107506 GENERAL INFORMATION:
                                                                                                                                                                                    XXXXXX
                                                                                                                                                                                        T 109
PCT-US91-07506-15 STANDARD; DNA; UNC; 858
                                                                                                                                                                                                                                       285 TTCTCAGAA 293
                                                                                             TITLE OF INVENTION: A TITLE OF INVENTION: CONTITLE OF INVENTION: CONTITUE OF SEQUENCES:
                                                                                                                                                                                                                              33 ttctcagaa 25
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Trecarcin, Richard F.
REGISTRATION NUMBER: 31.801
REFERENCE/DOCKET NUMBER: A-53469/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                 APPLICANT:
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                                                   STREET: 4 Embarcadero Center,
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER:
                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 94111
                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/346,333
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                                            USA
                                                                                                                                 Palzkill,
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                                                                                                                                 Botstein, David
Palzkill, Timothy
                                                                             Richard F.
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                                                                                                      Methods for modifying DNA and for detecting effects of such modification on encoded modified polypeptides with target
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                                                                   Trecartin
Center, Suite
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Pred. No. 3.96e+02
0; Mismatches
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RESULT 110
ID US-08-406-849-1 STANDARD; DNA; UNC; 861
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Best Local s
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Patent No. 5
GENERAL INF
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SEQUENCE 858 BP; 221 A; 205 C; 220 G;
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TELEFAX: 703-836-2787 INFORMATION FOR SEQ ID NO:
                                                                 APPLICATION NUMBER: US/08/406
FILING DATE: April 24, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 398-324
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Local Similarity 100.0%;
hes 9; Conservative
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                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: 700 South Washington Street, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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FILING DATE: 19911021
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: FEATURE:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                        STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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(415) TO NO: 15:
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GUILLOU-BONNICI, Francois
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                    703-836-2787
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Pred. No. 3.96e+02
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Matches
Query Match
               NAME/KEY: C
LOCATION: 1
SEQUENCE 871 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                    XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 ttctcagaa 25
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Local Similarity 100.0%;
les 9; Conservative
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                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 871 base pairs
TYPE: nucleic acid
                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,
                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-DEC-1993
                                                                                                                    REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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LENGTH: 861 base pairs
                                        FEATURE
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                                                MOLECULE TYPE:
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SOFTWARE: PatentI
                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                             TELEPHONE:
                                                        TOPOLOGY:
                                                               STRANDEDNESS: single
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: Californía
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Application US/08650578
                                                                                                                                                                                                                                                                                        901 California Avenue
                                                                                                      415-496-1200
                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                     Lanier, Lewis L
                                                                                                                                                                                                                                                                                                                                                              Aramburu Beltran,
                                                                                                                                                                                                                                                                                                                                             Phillips Jr
                                                                                                                                                                                                                                                                                                                                                                      Chang, Chiwen
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                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                       linear
                                                                                                                                                                                                                                                                                                DNAX Research Institute
                                                                                                              415-852-9196
                263 A; 168 C; 168 G;
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                                                                                                                                                                                                                                                                                                                       Related Reagents
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Pred. No.
 Score 9;
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3.96e+02;
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                 272 T; 0 OTHER.
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Length 871;
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PAtent No. 5258283.

Patent No. 5258283

Patent No. 5258283

PAPLICANT: FRAZIER, MARVIN

JAMES E.;BACA, OSWALD G.

TITLE OF INVENTION: DETECTI

BURNETII IN BIOLOGICAL FLUIDS

BURNER OF SEQUENCES: 17

CURRENT APPLICATION DATA:
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Matches . . 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application Sequence 3, Application Patent No. 5434058
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US-08-158-682A-3 STANDARD; DNA; UNC; 879
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Local Similarity 100.0%;
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                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coolley, Ronald B.
REGISTRATION NUMBER: 27,
                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                    STREET: 344
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 927,779
FILING DATE: 05-NOV-1986
APPLICATION NUMBER: 795,207
FILING DATE: 05-NOV-1985
                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/
FILING DATE: 23-OCT-1989
                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                              ARNOLD, WHITE & DURKEE 1 No. 5434058th Clark St
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US/08158682A
                                                                                                                                                                                                                                                                                                                                            Apolipoprotein B RNA Editing Protein: Composition and Method
                                                                                                                                      Release #1.0, Version
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                                                                                                         US/08/158,682A
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                ARCD: 085
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 879 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 114
US-08-801-740-4 STANDARD; DNA; UNC; 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 23..730
SEQUENCE 879 BP; 254 A; 207
 CLONE: Consensus
SEQUENCE 892 BP; 268 A; 192 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08801740
Sequence 4, Application US/08801740
                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                 INFORMATION FOR SEQ ID NO:
                    STRANDEDNESS: singl
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 TTCTGAGAA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 ttctgagaa 33
                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 892 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goli, Surya K.
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL P24 VESICLE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 Po:
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 94304
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Pred. No.
0; Misma
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  210 G; 221 T; 1 OTHER
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3.96e+02;
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Best Local S
Matches
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Sequence 9, Applicati
GENERAL INFORMATION:
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                     TELEFAX: 215-270-5090 INFORMATION FOR SEQ ID NO:
                                                                                               FILING DATE: 02-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION UNGMER: US 645
FILING DATE: 30-AUG-1984
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 149
FILING DATE: 05-NOV-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 013
FILING DATE: 01-FEB-1993
PRIOR APPLICATION NUMBER: US 108
APPLICATION NUMBER: US 108
FILING DATE: 18-AUG-1993
PRIOR APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                             APPLICATION NUMBER: US 8: FILING DATE: 18-FEB-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 7
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
                                            REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5096
                                                                                                                                                                     APPLICATION NUMBER: US 3 FILING DATE: 28-JUL-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                         FILING DATE: 30-AUG-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Vaccinal Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                             NAME: Baumeister, K: REGISTRATION NUMBER:
                                                                                                                                                APPLICATION NUMBER: US 2 FILING DATE: 02-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SmithKline Beecham Corporation ADDRESSEE: Patents
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Similarity 100.0%;
9; Conservative
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                                                                                         Baumeister, Kir
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Application PC/TUS9401149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scott, Miller
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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18-AUG-1993
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Pred. No. 3.96e+02
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                                                                    P50134
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Best Local Similarity 100.0%;
Matches 9; Conservative
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LOCATION: 1..918
SEQUENCE 918 BP; 295 A; 176 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58, Application Sequence 58, Application GENERAL INFORMATION:
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PCT-US94-01149-58 STANDARD; DNA; UNC; 918
                                                                                                     APPLICATION NUMBER: US 149
FILING DATE: 05-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 013
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 837
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 751
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 751
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genc
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 ttctcagaa 25
                                APPLICATION NUMBER: US 387,200
FILING DATE: 28-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 238,801
FILING DATE: 02-NOV-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Vaccinal Polypeptides NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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  ATTORNEY/AGENT INFORMATION:
            APPLICATION NUMBER: US 6 FILING DATE: 30-AUG-1984
                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19406-2799
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   King of Prussia
Pennsylvania
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U.S. Mailcode UW2220 - 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scott, Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shatzman, Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SmithKline Beecham Corporation - Corporate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Susan B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC/TUS9401149
PC/TUS9401149
                       US 645,732
                                                                                                                                                                     US 837,773
                                                                                                                                  US 751,896
                                                                                                                                                                                                       US 108,914
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Pred. No.
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE 918 BP; 292 A; 179 C; 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US96-03940-5 STANDARD; DNA; UNC; 928
                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 928 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 215-270-509
TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 TTCTCAGAA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                            HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 ttctcagaa 25
LIBRARY: CDNA
PUBLICATION INFORMATION:
AUTHORS: Chong, Jayho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5096
                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 520-3214
                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION NAME: Allen Bloom
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                  COMPUTER: IBM-compatible OPERATING SYSTEM: DOS 5.0 SOFTWARE: WordPerfect
                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. BO
                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: March
                                                                                                                 STRANDEDNESS:
                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                           REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                      ZIP: 08543-5218
                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                         : YEOTOGA
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                                                                                                                                                                                                                                                                                                                                                                                                            T: Mandel, Gail, Chong, Jayho
INVENTION: REST Protein and
F SEQUENCES: 29
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                                                                                                                                                                                                                                                                                                                                                         New Jersey
                                                                                                                                                                                                                                                                                                                                                                             P.O. Box 5218
                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                          linear
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                                                                                               cDNA to mRNA
                                                                                                                    double
                                                                                                                                                                                                                                                                                              DOS 5.0
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3, 1995
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Pred. No.
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Protein and DNA
                                                                                                                                                                                                                                                                                                                  3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                   317743-101
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Matches
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Matches
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Best Local
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Sequence 9, Application US/08632514C
Patent No. 5834234
GENERAL INFORMATION:
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US-08-632-514C-9 STANDARD; DNA; UNC;
                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 928 BP;
                 806
                                                                                                                         TELEFAX: (202)942-8484
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: WIXON, Henry N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)942-8459
33,
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TITLE OF INVENTION: APOPTOSIS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                     LENGTH: 958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
QUENCE 958 BP; 163 A; 314 C; 282
                                                                                                                                                                                                                                                                   ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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         TTCTCAGAA 814
ttctcagaa
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VOLUME:
ISSUE:
PAGES:
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AUTHORS:
TITLE: R
                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 29-MAY-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                            STREET: 1455 Pennsylva CITY: Washington, D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO:
NCE 928 BP; 363 A; 178 C; 182 G;
                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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Similarity 100.0%;
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Similarity 100.0%;
9; Conservative
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Yelena M., Frohman, Michael A., Kraner, Susan D.,
REST: A Mammalian Silencer Protein that Restricts
Sodium Channel Gene Expression to Neurons
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1455 Pennsylvania Avenue,
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                                 Score 9; DB 3; Le
Pred. No. 3.96e+02;
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Mandel, Gail
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RESULT

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Sequence 12, Application (
Sequence 12, Application (
Patent No. 5679546
GENERAL INFORMATION:
APPLICANT: Jone-Long (
APPLICANT)
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COUNTRY: US
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
CURRENT AP
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 999 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08, ETILING DATE: 03-JUL-1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/310
ETILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
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Local Similarity 100.0%;
hes 9; Conservative
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REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ric
STREET: 225 Franklin
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APPLICANT: Higgins, Paul J.
APPLICANT: Yeh, C. Grace
TITLE OF INVENTION: METHODS OF
TITLE OF INVENTION: ACTIVATION
                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                   NUMBER OF SEQUENCES:
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                                                      CURPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/24?
FILING DATE:
CLASSTTT
                                                                                                                                                                                                                       Sequence 2, Application US/08243543A
Sequence 2, Application US/08243543A
Patent No. 5614364
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         US-08-243-543A-2 STANDARD; DNA; UNC; 972 BP
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: cDNA
SEQUENCE 969 BP; 308 A; 224
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
TYPE: nucleic acid
Granuscausca 40:010
             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION UNMEER: 37,719
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338 INFORMATION FOR SEQ ID NO:
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Local Similarity 100.0%;
hes 9; Conservative
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REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/310,416A FILING DATE: 22-SEP-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: 111
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS/2 Model 50Z or 558X OPERATING SYSTEM: MS-DOS (Version 5.0) SOTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               APPLICANT: Tuggle, Christopher K
TITLE OF INVENTION: Genetic Mark
TITLE OF INVENTION: Production T
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CITY: [
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COUNTRY:
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801 Grand Avenue Suite 3200
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 972 BP;
                                                                                TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           851 TTCTCAGAA 859
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Local Similarity 100.0%;
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NAME/KEY:
LOCATION:
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NAME/KEY:
                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 987 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LENGTH: 972 base pairs
TYPE: nucleic acid
MOLECULE TYPE:
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ZIP: 943
                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
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                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                           350 Cambridge Avenue,
                                                                                                                                                                                                                                                                                                                                   USA
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CDNA to mRNA
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Pred. No.
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                       Query, Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                   TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 1000 BP; 340 A; 170 C; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/07965274 Sequence 3, Application US/07965274 Patent No. 5501947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE: Tc2.seq SEQUENCE 987 BP; 267 A; 223 C; 223 G; 274 T;
                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXXX
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US-07-965-274-3 STANDARD; DNA; UNC; 1000 BP.
 843 TTCTCAGAA 851
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Local Similarity 100.0%;
les 9; Conservative
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/GB91/01212
FILING DATE: 19-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9015845.2
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
ANALY. POSSENT
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TTCTGAGAA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WALKER, PATRICK TITLE OF INVENTION: METHOD TITLE OF INVENTION: REACTION OF INVENTION: REACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                    NAME: ROBINS, ROBERT REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0: FILING DATE: 12-MAR-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94301
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                       Score 9; DB 1; Length 1000; Pred. No. 3.96e+02; 0; Mismatches 0; Indels
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Pred. No.
0; Misma
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                                                                        259 T; 0 OTHER.
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Best Local s
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REFERENCE/DOCKET NUMBER: 3043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEPAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                           Sequence 1, Application Sequence 1, Application Patent No. 5569823
                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) SEQUENCE 1021 BP; 260 A; 246 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08459818 Sequence 17, Application US/08459818 Patent No. 5851795
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US-08-459-818-17 STANDARD; DNA; UNC; 1021
                                                                                                                                   T 125
US-08-247-809A-1 STANDARD; DNA; UNC; 1040 BP
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                                                                                                                          XXXXXX
         GENERAL INFORMATION:
APPLICANT: Peter H. Schreier; Klaus Stenzel;
APPLICANT: Edgar Maiss
TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          529 TTCTGAGAA 537
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Local Similarity 100.0%;
local 9; Conservative
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FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AGTIANO, Sarah B.
REGISTRATION NUMBER: 34,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSeq 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CTLA4 Receptor NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 11150 Sant
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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11150 Santa Monica Blvd.,
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Brady, William
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SPRUNG HORN KRAMER & WOODS
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US/08247809A
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Pred. No. 3.96e+02; 
0; Mismatches 0; Indels
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Best Local 9
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LOCATION: 36..989
SEQUENCE 1040 BP; 369 A; 186 C; 199
                                                                                                                                                                                                   Sequence 5, Application Sequence 5, Application Patent No. 5753479 GENERAL INFORMATION:
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US-08-843-521-5 STANDARD; DNA; UNC; 1047 BP.
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                          Match 100.0%;
Local Similarity 100.0%;
es 9; Conservative
                                                                                                                                 APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5753479el Compounds
NUMBER OF SEQUENCE: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: BETELECOMMUNICATION INFORMATION: TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0
MEDIUM TYPE: storage
COMPUTER: NEC Powermate 1 Plus
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 43 178 45.6 (Germany)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: May 28, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                             STREET: 709 Swedeland CITY: King of Prussia STATE: PA
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OPERATING SYSTEM:
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CITY: Tarrytown
STATE: New York
                                                                                        ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/247,809A FILING DATE: May 23, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
             APPLICATION NUMBER:
                                                                                                   COUNTRY:
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10591-5144
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                                                      IBM Compatible
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UMBER: US/08/843,521
18-APR-1997
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Pred. No. 3.96e+02
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        JT 127
US-07-940-605A-11 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Genomic DNA SEQUENCE 1047 BP; 284 A; 221 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1047 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9607993.4
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 931
REFERENCE/DOCKET NUMBER: P314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                           REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPAX: 212 869-8864/9741
                                                                                                                                  APPLICATION NUMBER: US/07
FILING DATE: 04-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                               APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
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             STRANDEDNESS:
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                   nucleic acid
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HOLLENBAUGH, DIAN
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             single
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Best Local Similarity 100.0%;
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     DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: '
SEQUENCE 1090 BP; 433 A; 206 C; 219 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1049 TTCTCAGAA 1057
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SEQUENCE 1060 BP;
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PCT-US96-03940-4 STANDARD; DNA; UNC; 1090
                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                   AYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: HeLa
IMMEDIATE SOURCE:
LIBRARY: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 ttctcagaa 25
                                                                PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapla-Ramirez Jos, Toledo-AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., *TITLE: REST: A Mammalian Silencer Protein that Restricts TITLE: Sodium Channel Gene Expression to Neurons
                                                                                                                                                                                                                                            NAME: Allen Bloom
REGISTRACION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 31'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 520-3214
                                                                                                                                                                                                                                                                                        FILING DATE: March 23, 1
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mandel, Gail, TITLE OF INVENTION: REST NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                              MOLECULE TYPE:
                      JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE: Ma
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PC:
FILING DATE: March 23,
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM-compatible OPERATING SYSTEM: DOS 5.0
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STREET: P
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Princeton
                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                               08543-5218
                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
: USA
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                                                Cell
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                                                                                                                                                                                                               1090 base pairs
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                                                                                                                                                                                        linear
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). Box 5218
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196 A; 349 C;
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PC/TUS9603940
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3, 1995
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Pred. No. 1
0; Mismat
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                                                                                                                                                                                                                                                                                                                                                               3.50 inch, 1.44 Mb storage
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3.96e+02;
       4:FROM 1 TO 1090; 232 T; 0 OTHER.
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Mandel, Gail
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                              Matches
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Best Local :
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US-08-592-126-95 STANDARD; DNA; UNC; 1093
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MEDIUM TYPE: Filoppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/592;126
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHAN: (415) 324-0960
INFORMATION FOR SEQ ID NO: 95:
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                                775 TICTGAGAA 783
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| 25 ttctgagaa 33
                                                                             Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gregory Dolganov TITLE OF INVENTION: Transcr
                                                                                                                                                                                     MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1093 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 350 Cam
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 4600-0111
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
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                                                              Conservative
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350 Cambridge Avenue, Suite 250
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Polypeptides
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US/08592126
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234 C; 249 G;
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                                                             Score 9; DB 3; Lo
Pred. No. 3.96e+02
0; Mismatches (
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Pred. No. 3.96e+02;
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                                                                                                                           304 T; 0 OTHER
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                                                                                           Length 1093;
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Sequence 2, Application US/08196350 Sequence 2, Application US/08196350 Patent No. 5585099

T 130 US-08-196-350-2 STANDARD; DNA; UNC; 1100

ВP

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Best Local S
Matches
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            STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application Sequence 4, Application Patent No. 5486463
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US-08-041-648-4 STANDARD; DNA; UNC; 1106
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NAME: GOSZ, WILLIAM G
REGISTRATION UNMBER: 27,787
REFERENCE/DOCKET NUMBER: GEN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617352786
TELEPAX: 6173747225
                                                                                                                                                                                                                                                                                                      APPLICANT: Lesslauer,
APPLICANT: L tscher,
APPLICANT: St ber, Di
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Local Similarity 100.0%;
les 9; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT: Moscicki, Richard
TITLE OF INVENTION: PROLACTIN AS ADJUVANT
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brad Salcedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02139
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STREET: 3
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CITY: Cambridge
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                                                                                                                                                                                                                                   E: George M. Gould,
340 Kingsland Street
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L tscher, Hansruedi
St ber, Dietrich
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US/08041648
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Pred. No. 3.96e+02.
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                           Version #1.25
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                       COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Rolesse #1.0, Version #1.25

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/08/041,648

FILING DATE: 1-APR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92810249.0

FILING DATE: 2-APR-1992

FILING DATE: 2-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application Sequence 6, Application Patent No. 5486463
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INFORMATION FOR SEQ ID NO: «
SEQUENCE CHARACTERISTICS:
LENGTH: 1106 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 TTCTGAGAA 387
                                                                                                                                                                                                                                                                               STATE: New Jersey
COUNTRY: U.S.A.
2IP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 ttctgagaa 33
  FILING DATE: 2-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: RATELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: N
ANTI-SENSE: NO
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PRIOR APPLICATION DATA:
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TITLE OF IN
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ATTORNEY/AGENT INFORMATION:
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ENCE 1106 BP; 305 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFOGUATION: LESSIAUER, Werner
NT: Lescher, Hansruedi
NT: St ber, Dietrich
DF INVENTION: TNF-MUTEINS
TROMPRICES: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pDS56/RBSII, SphI-THFalpha(Trp32)
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US/08041648
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ER: RAN 4105/147
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Pred.
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DB 1; Le 3.96e+02; 298 T; 0

Length 1106 0; Indels

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Hoffmann-La Roche Inc

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                                                                                      COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/041,648
FILING DATE: 1-APR-1993
CLASSIFICATION BATA:
APPLICATION NUMBER: EP 92810249.0
FILING DATE: 2-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: BCSGETAL CATHERING B
                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08041648 Sequence 8, Application US/08041648 Patent No. 5486463
                                                                                                                                                                                                                                                                                                                                                                                                        .T 133
US-08-041-648-8 STANDARD; DNA; UNC; 1106 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1106 BP; 305 A; 258 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 TTCTGAGAA 387
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1106 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (201) 235-35
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%;
Local Similarity 100.0%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 ttctgagaa
                           REGISTRATION NUMBER: 34240
REFERENCE/DOCKET NUMBER: RAN 4105/147
TELECOMMUNICATION INFORMATION:
-TELEPHONE: (201) 235-5208
TELEPAX: (201) 235-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34240
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1106 base pairs
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               APPLICANT: Lesslauer, Werner APPLICANT: L tscher, Hansruedi APPLICANT: St ber, Dietrich TITLE OF INVENTION: TNF-MUTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                             CITY: Nutley
                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 994..1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Plasmid pDS56/RBSII, SphI-TNFalpha(Ser29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                Roseman, Catherine R.
                                                                                                                                                                                                                                                                     340 Kingsland Street
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3.96e+02;
--hes 0;
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 994..1104
SEQUENCE 1106 BP; 305 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5631350
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 134
US-08-630-918-57 STANDARD; DNA; UNC; 1110
                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: APTLI 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: APTLI 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Walfen M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 TTCTGAGAA 387
                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: AN NUMBER OF SEQUENCES: 5
          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pair
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                               LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US
FILING DATE: APT11 5,
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LOCATION: 994..1104
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STRANDEDNESS:
 ORGANISM:
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805 Fifteenth
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 A2/A1ch1/2/68
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                    cDNA to genomic RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 C; 246 G;
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Street, N.W., #700
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Pred. No. 3.96e+02
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RESULT
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Best Local Similarity 100.0%;
Matches 9; Conservative
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US-08-229-781-57 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57,
Sequence 57,
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SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/0
FILING DATE: April 29, 1
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.1
COMPOTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTMARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/2
FILING DATE: APRIL 19, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                             FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A2/Aichi/2/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: AN NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                 ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                             MOLECULE TYPE:
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POSITION IN GENOME
                                                                                                                                                                                               HYPOTHETICAL:
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ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                        LIBRARY:
                                                           CELL TYPE:
                                                                                               HAPLOTYPE:
                                                                                                            DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                   STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                   TISSUE TYPE:
                                                                                                                                    STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                         INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                             nucleic acid
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Application US/08229781
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805 Fifteenth
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                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                           cDNA to genomic RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 C;
                                                                                                                                                                                                                                                                                                                                                                                                08/054,016
29, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/229,781
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Pred. No.
0; Misma
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Street, N.W.,
                                                                                                                                                                                                                                                                                    57
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3.96e+02;
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                   REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1129 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID
SEQUENCE 1110 BP; 374 A; 216 C; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9413187
Sequence 1, Application PC/TUS9413187
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US94-13187-1 STANDARD; DNA; UNC; 1129 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619 TTCTCAGAA 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
es 9; Conservative
                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WEI, ET AL.
TITLE OF INVENTION: Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHROMOSOME/SEGMENT: MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION
                                                                                                                                                                                                APPLICATION NUMBER: PCT/US94/13 FILING DATE: Submitted herewith
                                                                                                                                                                                                                                                                                                  COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CECCHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD:
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: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                               6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                             CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                            Human MutT2
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Pred. No. 3.96e+02
0; Mismatches
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Matches Query Match Best Local :

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RESULT '138
ID US-08-487-810-1 S
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                    TOPOLOGY: LINEAR MOLECULE TYPE: cDNA SEQUENCE 1129 BP; 333 A; 244 C; 258 G; 294 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08470261
Sequence 1, Application US/08470261
Patent No. 5695980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA
SEQUENCE 1129 BP; 333 A; 244 C; 258 G; 294 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-470-261-1 STANDARD; DNA; UNC; 1129
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION UMBER: PCT/US94/13187
APPLICATION NUMBER: PCT/US94/13187
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-372
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1094-1744
                                                                                                                 146 TTCTCAGAA 154
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                                                                                                                                                                                                                                                                                                         TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO:
                                                                                      33 ttctcagaa
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Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
FILING DATE: June 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WEI, ET AL.
TITLE OF INVENTION: Human MutT2
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: LINEAR MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1129 BASE PAIRS
                                                                                                                                                                                                                                                TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07068
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                            STANDARD; DNA; UNC;
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Pred. No. 3.96e+02
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ID US-08-456-104-3 STANDARD; DNA; UNC; 1151
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Best Local S
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GENERAL INFORMATION.

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

APPLICANT: Gray, Gary S.

APPLICANT: Gray, Gary S.

APPLICANT: Gray, Gary S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08456104 Sequence 3, Application US/08456104 Patent No. 5861310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
SEQUENCE 1146 BP; 459 A; 193 C; 238 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXX
         APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-UUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
AFTORNEY/AGENT INFORMATION:
NAME: MANGEMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 TTCTCAGAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 100.0%;
Local Similarity 100.0%;
les 9; Conservative
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                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1146 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                      STREET: 60 S
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO. 5618000
AL INFORMATION:
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US/08487810
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Pred. No. 3.96e+02;
0; Mismatches (
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Best Local :
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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LOCATION: 99..1028
SEQUENCE 1151 BP; 353 A;
                                         SEQUENCE 1151
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PCT-US95-02576-20 STANDARD; DNA; UNC; 1151
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                                                                                                                       TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
APPLICATION OF NOTE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 ttctcagaa 25
                                                                                                                                                                REFERENCE/DOCKET NUMBER: BY TELECOMMUNICATION INFORMATION TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  • LENGTH: 1151 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                       NAME/KEY: CDS
LOCATION: 99..1025
NCE 1151 BP; 353 A;
                                                                                                   STRANDEDNESS: double
                                                                                                                                                                                                NAME: Mandragouras, Amy E REGISTRATION NUMBER: 36,21
                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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Similarity 100.0%;
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Score 9; DB 4; Len Pred. No. 3.96e+02; 0; Mismatches 0;
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                                        C; 255 G;
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                                        285 T; 0 OTHER
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                   Length 1151;
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1108 TTCTCAGAA 1116
                                                                      SEQUENCE 1176 BP;
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SEQUENCE CHARACTERISTICS:
                                     Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                                                                                    APPLICATION NUMBER: 07/6
FILING DATE: 10-APR-91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07
FILING DATE: 09-JUL-91
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/237,937
APPLICATION NUMBER: 08/237,937
FILING DATE: 02-MAX-94
PRIOR APPLICATION NUMBER: 08/210,250
FILING DATE: 15-MAR-94
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordberfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                          NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07. FILING DATE: 09-DEC-91 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  FILING DATE: 15-MAR-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
ZIP: 021
                                                                                  TOPOLOGY: 11r
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                               LENGTH:
                                                                                                                                                                   TELEPHONE:
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                                                                                                    nucleic acid
                              Conservative
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                                                                                                                                                         (617) 542-5070
(617) 542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Trustees of Boston VENTION: ANTIBODIES TO VENTION: METHODS OF USE
                                                                   linear
P; 247 A; 333 C; 279 G;
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5 Franklin Street
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PC/TUS9503032
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                                                 Score 9;
                                        Pred.
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                              Mismatches
                                        9; DB 4; Lo
No. 3.96e+02
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INTERLEUKIN-8 RECEPTORS
                                                                      317 T; 0 OTHER.
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                                                 Length 1176;
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Best Local 9
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COMPUTER: ISBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/493,638
FILING DATE: 22-UUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00383/027001
TELEPHONE: 617/542-8906
TELEPHONE: 617/542-8906
                                                                                    Sequence 6, Application Sequence 6, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 80..374
SEQUENCE 1185 BP; 389 A; 234 C; 210 G;
                                                                                                                                   XXXXXX
                                                                                                                                               T 143
PCT-US95-07743-6 STANDARD; DNA; UNC; 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08493638 Sequence 5, Application US/08493638 Patent No. 5824299
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SEQUENCE CHARACTERISTICS:
LENGTH: 1185 base pairs
                                                                                                                                                                                                                    731 TTCTCAGAA 739
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                                                                                                                                                                                            33 ttctcagaa 25
                                                                                                                                                                                                                                        Match 100.0%;
Local Similarity 100.0%;
es 9; Conservative
TITLE OF INVENTION: NON-TOXIC, NON-TOXIGENIC, NOTITLE OF INVENTION: FUSARIUM EXPRESSION SYSTEM INUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVO NOTCISK OF NOTCH AMERICA, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MODULATION OF ENDOTHELIAL CELL TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Luster, Andrew APPLICANT: Leder, Philip
                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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ZIP: 02110-2804
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                                    NON-TOXIC, NON-TOXIGENIC, NON-PATHOGENIC FUSARIUM EXPRESSION SYSTEM AND PROMOTERS 16
                                                                                               PC/TUS9507743
PC/TUS9507743
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Pred. No. 3.96e+02
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                                                                                                                                                                                                                                                                                                                                                                                                               1031 TTCTCAGAA 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE 1188 BP; 366 A; 229
                                                                                                                                                                                                                                                                                                                              XXXXXX
                                                                                                                                                                                                                                                                                                                                          US-08-921-426-6 STANDARD; DNA; UNC; 1188 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/404,678
FILLING DATE: 15-MATCH-1995
ATTORNEY/AGENT INFORMATION:
NAME: AGY11s Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4216.204-W
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9655
TELEPAX: 212-878-9655
            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,426
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Local Similarity 100.0%;
tes 9; Conservative
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APPLICANT: Moyer, Donna L
APPLICANT: Yoder, Wendy T
APPLICANT: Shuster, Jeffrey R
TITLE OF INVENTION: NON-TOXIC, NON-TOXIGENIC, N
TITLE OF INVENTION: FUSARIUM EXPRESSION SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08 FILING DATE: 30-June-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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                                                                                                                                                                      NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
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PRIOR APPLICATION DATA:
                                                                                                CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 10174-6401
                                                                                                                                               STREET:
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   FILING DATE:
                                                                                                                                                           ADDRESSEE:
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P; 366 A; 229 C;
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IBM PC compatible
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                                                                                                                                                                      ADDRESS
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   29-AUG-1997
                                                                                                                                                            58378470 No.
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Pred. No. 3.96e+02
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e, 64th Floor
                                        Version #1.
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Best Local S
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                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: AGIIS Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE 1188 BP; 366 A; 229 C; 252 G; 341 T; 0 OTHER
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US-08-592-126-56 STANDARD; DNA; UNC;
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GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08//
FILING DATE: 01-JUN-1995
FILING DATE: 15-MAR-1995
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Local Similarity 100.0%;
nes 9; Conservative
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                                                                                                                                                                                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts F
TITLE OF INVENTION: Polypeptides
NIMBER OF SEQUENCES: 151
                                                                        SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: HYPOTHETICAL:
                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              ZIP: 94306
                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                              STREET: 350 Campa CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dehlinger & nosuccest 250 STREET: 350 Cambridge Avenue, Suite 250
                                                             LENGTH:
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                                                             1189 base pairs
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: cDNA to mRNA
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Pred. No. 3.95e+02;
0; Mismatches (
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US-08-864-799-2 STANDARD; DNA; UNC; 1196
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                                                        SEQUENCE 1196 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXX
830 TTCTGAGAA 838
                                                                                                                                           TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
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Local Similarity 100.0%;
ses 9; Conservative
                                                    IMMEDIATE SOURCE:
LIBRARY: ENDCHOOTO1
CLONE: 2134944
OUENCE 1196 BP; 338 A; 221
                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1196 base pair
                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                 STATE: C
                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: Filed CLASSIFICATION: 435
                                                                                             STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                          NAME: Billings, Lucy REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION:
                                                                                                               TYPE: nucleic acid
                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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                  Similarity 100.0%;
Similarity 100.0%;
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    Application US/08864799
    Application US/08864799
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                                                                                                                        1196 base pairs
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Shah, Purvi
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281 C; 235 G;
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Pred. No. 3.96e+
0; Mismatches
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                 Score 9;
Pred. No.
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                                                        275 G;
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). 3.96e+02
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3.96e+02
                                                        362 T;
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                                   Length 1196;
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                                                       0 OTHER.
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                                                                                                                            Sequence 2, Application US/08334639 Sequence 2, Application US/08334639 Patent No. 5536653
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Sequence 1, Application US/08434881
Patent No. 5804376
GENERAL INFORMATION:
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US-08-434-881-1 STANDARD; DNA; UNC; 1221 BP
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SEQUENCE 1221 BP; 412 A; 210 C; 249 G; 337 T; 13 OTHER.
                                                                                                                                                                                                                          XXXXXX
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                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   659 TTCTGAGAA 667
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION UNMER: 33954
REFERENCE/DOCKET NUMBER: PFOOTELEOMNUNICATION INFORMATION:
TELEPHONE: 415-852-0195
TELEFAX: 415-852-0195
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                       APPLICANT:
APPLICANT:
APPLICANT:
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Local Similarity 100.0%;
es 9; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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APPLICANT: Wilde, Cra
APPLICANT: Diep, Dinh
  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: Californi
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                      LIBRARY:
CLONE: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: Herewi CLASSIFICATION: 435
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LOCATION: 1...
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TOPOLOGY: 11
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                Barry, Gerard F.
Edwards, Janice W.
Kishore, Ganesh M.
Stark, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1221 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Braxton, Scott M. Wilde, Craig G.
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  Tomato Fruit Promoters
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Pred.
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3.96e+02;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1226 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Barry, Ger
APPLICANT: Kishore, G
APPLICANT: Stark, Dav
TITLE OF INVENTION: E
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1135 TTCTCAGAA 1143
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Sequence 26, Application US/08090523
Patent No. 549830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JT 149
US-08-090-523-26 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) SEQUENCE 1226 BP; 378 A; 236 C;
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                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/090,52: FILING DATE: 19930712 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TELEPHONE: (314)537-7286
TELEFAX: (314)537-6047
                                                                                                                                                                                                                                                             STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: Grace L. Bonne
STREET: 700 Chesterfield
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: St. Louis
STATE: Missouri
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REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                    63198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barry, Gerard F
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field Parkway No. 5498830th
  us 07/709663
                                                                                      US/08/090,523
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field Parkway No.
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Pred. No. 3.96e+02
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5536653th
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Best Local
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 1226 BP; 378 A; 236 C; 203 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/08398627
Sequence 26, Application US/08398627
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US-08-398-627-26 STANDARD; DNA; UNC; 1226 BP
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,523
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
PRIOR APPLICATION NUMBER: US 07/539763
APPLICATION NUMBER: US 07/539763
APPLICATION INFORMATION:
NAME: Bonner, Grace L.
NAME: Bonner, Grace L.
REGISTRATION NUMBER: 38-21(10559)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314).537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
TELEPAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                         COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPUTER: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1226 base pairs
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh
APPLICANT: Stark, David M.
TITLE OF INVENTION: Enhance
                                                                                                                                                                          APPLICATION NUMBER: US/08/398,627 FILING DATE: 03-MAR-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bonner, Grace REGISTRATION NUMBER:
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Similarity 100.0%;
9; Conservative
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)O Chesterfield Parkway No. 560
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Pred. No.
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3.96e+02
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   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local :
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 1226 BP; 378 A; 236 C; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1135 TTCTCAGAA 1143
                                                  MOLECULE TYPE: cDNA
SEQUENCE 1227 BP; 320 A; 288 C; 265 G; 353 T; 1 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5824306 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09031485
Sequence 18, Application US/09031485
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US-09-031-485-18 STANDARD; DNA; UNC; 1227
                                                                                           TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 nucleotides
TYPE: nucleic acid
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
ETILING DATE:
FILING DATE:
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                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPHONE: 970/493-7272
TELEPHONE: 970/493-7272
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Local Similarity 100.0%;
les 9; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado COUNTRY: USA
                                                                         STRANDEDNESS:
TOPOLOGY: 11:
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Blehm, E. Sc
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Pred. No.
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              Score 9; DB 3; L
Pred. No. 3.96e+02
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3.96e+02;
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 GENERAL INFORMATION:
ARPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scc
TITLE OF INVENTION: DIRC
TITLE OF INVENTION: PROJ
TITLE OF INVENTION: USES
                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09031485
Sequence 17, Application US/09031485
Patent No. 5824306
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                                                                                                               .T 153
US-09-031-485-17 STANDARD; DNA; UNC; 1227
                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
SEQUENCE 1227 BP; 320 A; 288 C; 265 G; 353 T; 1 OTHER.
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                                                                                                                                                      916 TTCTGAGAA 924
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| 25 ttctgagaa 33
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                                                                                                                                                                                                      y Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                            TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: HW-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPHONE: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1227 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Carol Talkington Verser, ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                            linear
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  DIROFILARIA AND BRUGIA ANKYRIN PROTEINS, NUCLEIC ACID MOLECULES, USES THEREOF
                                                                                                                                                                                                        Score 9;
Pred. No.
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Best Local S
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US-08-847-429A-17 STANDARD; DNA; UNC; 1227 BP.
                                                                                                                                                                                                                                                                                                    XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/847,42:
APPLICATION NUMBER: US/08/847,42:
APPLICATION INFORMATION:
NAME: Verser Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HH-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                     304 TTCTCAGAA 312
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TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Local Similarity 100.0%;
hes 9; Conservative
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MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                       COMPUTER READABLE FORM:
                                                                                                                                                                            TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                APPLICANT: Tang, Liang APPLICANT: Blehm, E. S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
                                                                                                     ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Carol Talkington Verser, ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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Matches
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US-09-031-485-16 STANDARD; DNA; UNC; 1228 BP.
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE 1227 BP: 353 A; 265 C; 288 G;
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Sequence 16, Application US/09031485
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APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
          TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
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Local Similarity 100.0%;
es 9; Conservative
                                          NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
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                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         SOFTWARE: WordPerfect for Windows, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1227 nucleotides
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                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                       FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CCITY: Fort Collins
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                                                                                                                                                                                                                                                                                         STATE:
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                               970/484-9505
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Pred. No.
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                       Matches
                                                                                                                             Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                         MOLECULE TYPE: cDNA
SEQUENCE 1228 BP; 320 A; 288 C; 266 G; 353 T; 1 OTHER.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429A
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE 1228 BP; 320 A; 288 C; 266 G; 353 T; 1 OTHER.
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                                                   917 TTCTGAGAA 925
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1228 nucleotid
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APPLICANT: Blehm, E. Sco
TITLE OF INVENTION: DIR
TITLE OF INVENTION: USE:
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CORRESPONDENCE ADDRESS:
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ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
  ttctgagaa 33
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                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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                                                                                                       9;
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                                                                                                                             Score 9;
Pred. No.
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Pred. No.
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                                                                                                          Mismatches
                                                                                                                                  No.
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. 3.96e+02;
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                                                                                                          Indels
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RESULT ID US

JT 157 US-09-031-485-14 STANDARD; DNA; UNC; 1228 BP

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Best Local
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GENERAL INFORMATION:

APPLICANT: Tang, Lia
APPLICANT: Blehm, E.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:
                                                             Sequence 14, Application US/08847429A Sequence 14, Application US/08847429A Patent No. 5827692
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GENERAL INFORMATION:
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                                                                                                                     US-08-847-429A-14 STANDARD; DNA; UNC; 1228
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/847,42:
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REGISTRATION NUMBER: 37,459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DIROFILARIA
TITLE OF INVENTION: PROTEINS, NU
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: HW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
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ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
                                                                                                                                                                                                                                                                                                      STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 1...
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Blehm, E. Scot
                              Tang, Liang
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           DIROFILARIA AND BRUGIA PROTEINS, NUCLEIC ACID
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  USES THEREOF
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Best Local 8
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Sequence 4, Application PC/TUS9303077
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 1228 BP; 353 A;
                                                                                                                                                                                                                                                               XXXXX
                                                                                                                                                                                                                                                                         PCT-US93-03077-4 STANDARD; DNA; UNC; 1242
                                                                                                                                                                                                                                                                                                                                        304 TTCTCAGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                              y Match 100.0%;
Local Similarity 100.0%;
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                    33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: HW TELECOMMUNICATION INFORMATION: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                    APPLICANT: Gaynor, Richard B. APPLICANT: Wu, Foon Kin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1228 nucleotid
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                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1825 Sharp
CITY: Fort Collins
STATE: Colorado
                                                                                                          CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1..1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Carol
ADDRESSEE: Heska
  APPLICATION NUMBER:
                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                 ADDRESSEE:
                                                                           77210
                                                                                     Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Carol Talkington Verser,
E: Heska Corporation
1825 Sharp Point Drive
                                                                                                                       P.O. Box 4433
                                                                                                                                                                                                          Board of Regents, The University of Texas System
                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                Arnold White & Durkee
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  PCT/US93/03077
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Pred. No.
0; Misma
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
                                                               266 C; 288 G; 320 T; 1 OTHER
                 DB 3; Le
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Best Local Similarity 100.0%;
Matches 9; Conservative
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PCT-US95-02576-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown SEQUENCE 1242 BP; 479 A; 215 C; 295 G; 253 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                       Sequence 12, Application Sequence 12, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        XXXXXX
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1242 base pair
LENGTH: TOTETC ACID
                                                   TELEFAX: (617)227-594
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                 15 TTCTGAGAA 23
                                                                                                                                                                                                                                                                                                                                                                                25 ttctgagaa 33
                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/205,697
APPLICATION NUMBER: 02-Mar-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/862,025
FILING DATE: April 2, 1992
                                                                 NAME: Mandragouras, Amy E.
REGISTATION NUMBER: 36,227
REFERENCE/DOCKET NUMBER: BW:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: UTFD270PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1540
                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                SEQUENCE CHARACTERISTICS:
LENGTH: 1261 base pair
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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NAME: Kammerer Datrice
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STREET: ...
TITY: Boston
Tity: "Assar
STRANDEDNESS:
TOPOLOGY: ling
OLECULE TYPE:
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                                                                                                                                                                                                               ZIP: 02109-1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
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CLASSIFICATION:
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                        1261 base pairs ucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713-749-2679
                                                         (617)227-5941
         linear
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PC/TUS9502576
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Pred. No. 3.96e+02;
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RESULT
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NAME/KEY: CD:

LOCATION: 194

SEQUENCE 1261 BP;
                                                                                                                                                                                                                       TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1273 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
        .T 162
US-07-794-731A-2 STANDARD; DNA; UNC; 1273 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/07794731A Sequence 1, Application US/07794731A
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US-07-794-731A-1 STANDARD; DNA; UNC; 1273
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XXXXXX
                                                                                                                                                                                                          SEQUENCE 1273 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/794,731A
FILING DATE: 19911115
                                                                                                             663 TTCTCAGAA 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             etent No. 5348867
GENERAL INFORMATION:
                                                                               33 ttctcagaa 25
                                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
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Local Similarity 100.0%;
Local Similarity 100.0%;
Tes 9; Conservative
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ATTORNEY AGENT INFORMATION:
NAME: Kitchell, Barbara S.
NAME: Kitchell, Barbara S.
NAME: ATTORN NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: GE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. B
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LE OF INVENTION:
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P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Joseph A. Francisco
Charles F. Earhart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
194..1135
BP; 358 A; ;
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                                                                                                                                                                                                          339 A; 308 C; 332 G; 294 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression of Proteins on Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 9;
Pred. No.
                                                                                                                                                         Score 9; DB 1; L
Pred. No. 3.96e+02
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                                                                                                                                             Mismatches
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3.96e+02
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                                                                                                                                                                          Length 1273;
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Application US/07794731A

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1273 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear SEQUENCE 1273 BP; 339 A; 308 C; 332 G; 294 T; 0 OTHER
                                                                                                                                                                                                                                       Sequence 28, Application PC/TUS9603940 Sequence 28, Application PC/TUS9603940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    XXXXXX
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Patent No.
                                                                                                                                                                                                                                                                                                          T 163
PCT-US96-03940-28 STANDARD; DNA; UNC; 1284
                                                                                                                                                                                                                                                                                                                                                                                   663 TTCTCAGAA 671
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                                                                                                                                                                                                                                                                                                                                                                     33 ttctcagaa
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC'
                                                                  ZIP: 08543-5218
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19911115
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: George Georgiou
APPLICANT: Joseph A. Francisco
APPLICANT: Charles F. Earhart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Expression of Proteins on Bacterial TITLE OF INVENTION: Surface
                                                                                                                                                                                                              APPLICANT: Mandel, Gail, Chong, Jayhong A. TITLE OF INVENTION: REST Protein and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Texa
COUNTRY: US
ZIP: 77210
                                         COMPUTER: IBM-compatible OPERATING SYSTEM: DOS 5.0
                                                                                                                                          CITY: Princeton
                                                                                                                                                      STREET: P.O. Box 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                           COUNTRY:
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5. 5348867
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                                                                                                                           New Jersey
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                                                                                                              USA
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 PCT/US96/03940
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Pred. No. 3.96e+02;
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                                                                     1.44 Mb storage
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ID US-08-906-744A-1 STANDARD; DNA; UNC; 1290
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                33 ttctcagaa
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PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
PUBLICATION Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C.,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D.,
TITLE: REST: A Mammalian.Silencer Protein that Restricts
SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,744A
                                                                                                                                                                                               APPLICANT: Gentry, Daniel APPLICANT: Greenwood, Rebecca APPLICANT: Lawlor, Elizabeth TITLE OF INVENTION: NOVEL hiss NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 520-3214
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Allen Bloom
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1284 base par
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                 STREET: 709 Swederaum
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: M
CLASSIFICATION:
                                         COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 100.0%;
Similarity 100.0%;
9; Conservative
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                                                                                               19406-0939
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Altschuler, Mandel, Gail

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                                      FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SPITALS, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 1920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9412912
Sequence 3, Application PC/TUS9412912
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  1249 TTCTCAGAA 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Genomic RNA SEQUENCE 1290 BP; 367 A; 290 C;
                                                                                                                                                                                                                                                                                                                              PCT-US94-12912-3 STANDARD; DNA; UNC; 1296
                                                                                                                                                                                                                                                                                                                       XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1290 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                  33 ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%;
Local Similarity 100.0%;
les 9; Conservative
                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9607
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                       SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
                                                                                                                                                                                                STREET: 201 ...
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
aDDRESSEE: c/o Robbins, Berliner & Carson
                                                                                                                                                                                                                                                           APPLICANT: UNIVERSITITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                        COUNTRY:
ZIP: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 0 CLASSIFICATION:
       STRANDEDNESS:
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               nucleic acid
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                       Query Match
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Matches
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       1039 TTCTGAGAA 1047
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Query Match
Best Local Similarity 100.0%;
                                                         OTHER INFORMATION:
OTHER INFORMATION:
SEQUENCE 1328 BP; 377 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: SEQUENCE 1296 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 166
US-07-679-052A-14 STANDARD; DNA; UNC; 1328
                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: PATENTIN Release #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679.
FILING DATE: 19910506
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 TTCTGAGAA 450
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                                                                                                                                  NAME/KEY:
LOCATION:
FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BUNN, Clive L.
TITLE OF INVENTION: RECOMBINANT PRODUCT
NUMBER OF SEQUENCES: 17
                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                           TOPOLOGY: linear
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h 100.0%;
Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUNN, Clive L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RICHARDSON,
                                                                                                                                                  CDS
15..1319
                                                                                                         sig_peptide
15..71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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372 A;
                                                                                                                                                                                             Other nucleic acid;
Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peter L.
                                                         /product- "Synthetic signal peptide" 300 C; 317 G; 334 T; 0 OTHE
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US/07679052A
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Score 9;
Pred. No.
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. 3.96e+02;
                 DB 1; Le
3.96e+02;
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                           Length 1328;
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   Indels
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Foley & Lardner

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RESULT 168
ID US-07-679-052A-16 STANDARD; DNA; UNC; 1340
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Best Local :
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                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 3288
REFERENCE/DOCKET NUMBER: 3288
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
TROPMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pairs
                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 9..803
SEQUENCE 1338 BP; 421 A; 244 C; 333 G; 340 T; 0 OTHER.
                                                       Sequence 16, Application Sequence 16, Application Patent No. 5298400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/07651710A
Sequence 1, Application US/07651710A
Patent No. 5362864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /T 167
US-07-651-710A-1 STANDARD; DNA; UNC; 1338 BP.
                                                                                          XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xxxxxx
       GENERAL INFORMATION:
APPLICANT: WHITFELD, Peter L.
APPLICANT: RICHARDSON, Michael A.
'APPLICANT: BUNN, Clive L.
TITLE OF INVENTION: RECOMBINANT PRODUCT
NUMBER OF SEQUENCES: 17
                                                                                                                                          395 TTCTGAGAA 403
                                                                                                                                                                  / Match 100.0%;
Local Similarity 100.0%;
nes 9; Conservative
                                                                                                                                  25 ttctgagaa 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 ttctgagaa
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/651,710A
FILING DATE: 19910206
CLASSIFICATION: 800
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                            MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Trans-Activating Factor-1 NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                             STRANDEDNESS: sin TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                             NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chua, Nam-Hai
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                                                                US/07679052A
US/07679052A
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Pred. No.
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No. 3.96e+02
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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NAME/KEY: Sig_peptide
LOCATION: 15..86
OTHER INFORMATION: /product= "a-1-antitrypsin signal"
SEQUENCE 1340 BP; 374 A; 308 C; 317 G; 341 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/08385745
Sequence 26, Application US/08385745
Patent No. 5612209
                                                                                                                                                                                                                                                                                                                                                                                                       XXXXXX
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US-08-385-745-26 STANDARD; DNA; UNC; 1341
                             CITY: New York
STATE: New York
STATE: U.S.A.
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 ttctgagaa 33
                                                                                                                                                                                                                             APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and R
TITLE OF INVENTION: Vespid Venom I
TITLE OF INVENTION: Based Thereon
                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19910506
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley
STREET: 1800 Diag
CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1340 base pai
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patent:
   OPERATING SYSTEM:
                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1340 base pairs
                                                                                                                                                    3: Pennie & Edmonds
1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
15..1331
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IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               Cloning and Recombinant Production of Vespid Venom Phospholipases, and Immu
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Pred. No. 3.96e+02;
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Sequence 26, Applicat
GENERAL INFORMATION:
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PCT-US94-02629-26 STANDARD; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1341 BP; 473 A; 206 C; 239 G; 423 T; 0 OTHER.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02629
FILING DATE: 10-MAR-1994
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/180,209
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq.; David A.
                                                                                                                                                                                                                                                                                                                               XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 328
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
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Local Similarity 100.0%;
les 9; Conservative
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TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASEL
NUMBER OF SEQUENCES: 62
                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/385,745; FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                STREET: 411 Hack
CITY: Hackensack
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LOCATION: 153..1052
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                                                                                                                                                                    07601
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Application PC/TUS9402629
                                                                                                                                                                                         New Jersey
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                                                                                                                     PatentIn Release #1.0, Version #1.25
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Pred. No. 3.96e+02;
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            IELEX: 13521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 bacc
Type
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                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 55938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  819 TTCTCAGAA 827
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                                                   TELEPHONE: ZU1 TO TELEPHONE: ZU1 TO TENAX: 201 343-1684
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TOPOLOGY: 11
    TYPE: nucled STRANDEDNESS:
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NAME/KEY: CDS
LOCATION: 153..1052
SEQUENCE 1341 BP; 473 A; 206 C;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
Match 100.0%;
Local Similarity 100.0%;
ses 9; Conservative
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                         LENGTH: 1341 base pairs
                                                                                                                  CDNA
                                                                                                                                             single
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Score 9;
Pred. No.
0; Misma
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                                                         239 G; 423 T; 0
 Mismatches
               DB 4; Le 3.96e+02;
                         Length 1341;
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                                                         OTHER
   Indels
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/T 171 US-08-180-209B-26 STANDARD; DNA; UNC; 1341 BP US/08180209B US/08180209B

APPLICANT: King, Te-TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: Te-Piao CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASE THEREON

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: Klauber & Jackson

ZIP: 07601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk STREET: 411 Hacker CITY: Hackensack STATE: New Jersey COUNTRY: USA New Jersey 411 Hackensack Avenue Release #1.0, Version

COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,209B
FILING DATE: 11-MAN-1994
CLASSIFICATION: 435.
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
11-MAR-1993
ATTORNEY/ACENT INFORMATION:
NAME: JECKSOR ESG. DAVIG A NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26.742 REFERENCE/DOCKET NUMBER: 600 TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800 US/08/180,209E 600-1-074 CIP

1341 base pairs 26:

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                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                        NAME/KEY: CDS
LOCATION: 1..1353
SEQUENCE 1353 BP; 461 A; 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08625322
Sequence 3, Application US/08625322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-625-322-3 STANDARD; DNA; UNC; 1353
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LOCATION: 153..1052
SEQUENCE 1341 BP; 473 A; 206 C; 239 G; 423 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 580441;
                     961 TTCTCAGAA 969
                                                                                                                                                                                               TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,322
FILING DATE: 01-APR-1996
CLASSIFICATION: 435
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MOLECULE TYPE:
FEATURE:
  33 ttctcagaa 25
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1353 base pairs
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gill, Gordon N.
APPLICANT: Kurten, Richard C.
APPLICANT: Cadena, Deborah L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FITLE OF INVENTION:
                                                                                                                                       STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                  California
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4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                         USA
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01-APR-1996
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Pred. No. 3.96e+02,
0; Mismatches (
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Pred. No. 3.96e+02
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                                                                                          304 G;
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                                                                  Length 1353;
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                                                   Sequence 3, Application PC/TUS9603940 Sequence 3, Application PC/TUS9603940 GENERAL INFORMATION:

APPLICANT: Mandel, Gail, Chong, Ja
                                                                                                                                                                                                                                                 MOLECULE TYPE: cDNA
SEQUENCE 1375 BP; 363 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08736723A Sequence 1, Application US/08736723A Patent No. 5869235
                                                                                                          XXXXXX
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APPLICANT: SUDA,
APPLICANT: ITOGA,
                                                                                                                                                                                   102 TTCTCAGAA 110
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pair:
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-3
FILING DATE: 28-DbC-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24 61
REFERENCE/DOCKET NUMBER: 2
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Local Similarity 100.0%;
les 9; Conservative
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SOFTWARE: PATEUL...
CURRENT APPLICATION NUMBER: US/08
APPLICATION NUMBER: US/08
APPLICATION 125-0CT-1996
                 TITLE OF INVENTION: RE NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                   STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: JP 7 FILING DATE: 27-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
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          DDRESSEE:
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P.O. Box 5218
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1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
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SYSTEM: PC-DOS/MS-DOS
          Dechert Price & Rhoads
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                                          REST Protein and
                                                                                                                                                                                                                                                  282 C; 382 G;
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Pred. No. 3.96e+02;
0; Mismatches (
                                                   Chong, Jayhong
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RELEVANT RESIDUES IN SEQ ID NO: SEQUENCE 1407 BP; 515 A; 276 C; 306 G;
                                                                              Sequence 1, Application Sequence 1, Application Patent No. 5650501
                                                                                                                         T 175
US-08-252-995D-1 STANDARD; DNA; UNC; 1453 BP
                                                                                                                 XXXXXX
                                          GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (609) 520-3214
TELEFAX: (609) 520-3259
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,135
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 3177
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (609) 520-3214
TELEPHONE: 700-70-3259
                                                                                                                                                                             724 TTCTCAGAA 732
                                                                                                                                                             33 ttctcagaa 25
                                                                                                                                                                                               Match 100.0%;
Local Similarity 100.0%;
les 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                            LIBRARY: CDNA
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT NAME: Allen
                 CORRESPONDENCE ADDRESS:
                          TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                   NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Princeton
STATE: New Jers
COUNTRY: USA
                                                                                                                                                                                                                                                                                               AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos, Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C.,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D.,
TITLE: REST: A Mammalian Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: March CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM-compatible OPERATING SYSTEM: DOS 5.
                                                                                                                                                                                                                                                                               VOLUME:
                                                                                                                                                                                                                                                                                       JOURNAL:
          ADDRESSEE:
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E: BERESKIN & PARR 40 King Street West
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                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   double
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US/08252995D
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Mandel, Gail
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               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM-compatible
OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
 SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KURDYDK, Linda M
REGISTRATION NUMBER: 34,971
REGISTRATION NUMBER: 34,971
                                                                                                           Sequence 27, Application PC/TUS9603940 Sequence 27, Application PC/TUS9603940 GENERAL INFORMATION:
                                                                                                                                                                                                         T 176
PCT-US96-03940-27 STANDARD; DNA; UNC; 1461 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..205
SEQUENCE 1453 BP; 426 A; 315 C; 357 G; 355 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (416) 361-139
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Local Similarity 100.0%;
les 9; Conservative
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MEDIUM TYPE: Floppy disk
                                     NUMBER OF SEQUENCES: 2
                                                                          APPLICANT: Mandel, Gail, Chong, Jayhong A. TITLE OF INVENTION: REST Protein and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
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IMMEDIATE SOURCE:
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P.O. Box 5218
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Pred. No. 3.96e+02
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Sequence 5, Application US/07768286B
Patent No. 5444153
GENERAL INFORMATION:
APPLICANT: GOSS, Neil H.
APPLICANT: RICHARDSON, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE 1461 BP; 528 A; 288 C; 326
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TELEFAX: (609) 520-329
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pairs
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Local Similarity 100.0%;
hes 9; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/768,286B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: cDNA
PUBLICATION INFORMATION:

AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C.,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D.,
TITLE: REST: A Mammalian Silencer Protein that Restricts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGI.
MOLECULE TYPE: cD
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REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                          TITLE OF INVENTION: VARIANTS NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Allen Bloom
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TITLE: Sodi
JOURNAL: Ce
VOLUME: 80
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                                                                                                           CITY: Alexandria
STATE: Virginia
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CELL LINE: HeLa
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STRANDEDNESS: double
                                                                                                COUNTRY:
                                                                                                                                                   ADDRESSEE:
                                                                                     ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sodium Channel Gene Expression to Neurons
                                                                                                                                    1800 Diagonal Road,
                                                                                                 USA
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23, 1995
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Pred. No.
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3.96e+02;
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Mandel, Gail
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Best Local Similarity 100.0%;
Matches 9; Conservative
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APPLICANT: Synaptic Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 1482 BP;
                                                                                                                                                                                                                                                 PCT-US95-15646-1 STANDARD; DNA; UNC; 1501
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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ORGANISM: Homo
                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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CLONE: BTA 1922
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                                     ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 22..1170
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                 COUNTRY:
                                                                                                 ADDRESSEE:
                                                             New York
                                                                                     E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĕ
                                                                                                                                      Synaptic Pharmaceutical Corporation
ENTION: METHODS OF MODIFYING FEEDING BEHAVIOR, COMPOUNDS
ENTION: USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC
VENTION: Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF
                                                 United States
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FILING DATE: 19911011
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.76
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1482 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                          (703)683-4109
                                                                                                                                                                                                         Homo sapiens
                                                                                               OD: experimental
/function= "Product binds to
urokinase, tissue plasminogen activator"
/product= "PAI-2 variant, protease sensitive
                                    /evidence- EXPERIMENTAL /note- "Codes for human plasminogen activator inhibitor type 2 protein in which amino acids to 98 inclusive have been deleted."
307 C; 320 G; 416 T; 0 OTHER.
                                                                                       removed"
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                                                                                                                                                                                                                                                                                                                                                                29,768
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Score 9; DB 1; Length 1482 
Pred. No. 3.96e+02; 
0; Mismatches 0; Indels
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APPLICANT: Gerald,
APPLICANT: Walker,
APPLICANT: Branche
                                                                                                                                                                                                                                             Sequence 1, Application US/08349025
Sequence 1, Application US/08349025
Patent No. 5602024
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 61..1432
SEQUENCE 1501 BP; 400 A;
                                                                                                                                                                                                                                                                             xxxxxx
                                                                                                                                                                                                                                                                                     US-08-349-025-1 STANDARD; DNA; UNC; 1501
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TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                   10 TTCTGAGAA 18
                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,
                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/349,02
                                                                                                                                                                              TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1501 base pairs
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                                                                                                                                              STREET:
CITY: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: PatentI
                                                FILING DATE: CLASSIFICATION: 514
                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             COUNTRY:
                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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Similarity 100.0%;
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Walker,
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Weinshank, Richard L.
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n Release #1.0, Version
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45R: 1795/46166-A-PCT
                                                                US/08/349,025
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Pred. No.
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3.96e+02;
                                                                                Version #1.25
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RESULT
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1510 base
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LOCATION: 61..1432
SEQUENCE 1501 BP; 400 A;
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Sequence 1, Application PC/TUS9207103
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/0710
                                                                                                                                                                             FILING DATE: 23-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BYOOK, DAY'IG E
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
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                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 23-AUG-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Massachusetts Institute of Technology; Forsyth Dental APPLICANT: Center and Ohio State University TITLE OF INVENTION: NOVEL STRAIN OF CHLAMYDIA NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: ADDRESS: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
               MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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STRANDEDNESS: sing
                                                                             LENGTH: 1510 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                               TOPOLOGY:
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ID NO: :
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Pred. No. 3.96e+
0; Mismatches
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3.96e+02;
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ORGANISM:

Chlamydia sp

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Best Local :
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                                                                                                                                                                                                                                                                                                                                            Patent No. 5444153
GENERAL INFORMATION:
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US-07-768-286B-3 STANDARD; DNA; UNC; 1512
                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 1510
                                                          INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
APPLICATION NUMBER: POT/AU
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                                                                        25 ttctgagaa 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%;
Local Similarity 66.7%;
mes 6; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: Stills Jr., Harold F.
TITLE: Isolation of an Intracellular Bacterium
                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                         TELEFORMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 UUCUGAGAA 9
                                     HYPOTHETICAL:
                                            TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                      APPLICANT: GOSS, Neil H. APPLICANT: RICHARDSON, MITTLE OF INVENTION: VARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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                                                                                                                                                                                      APPLICATION NUMBER: U FILING DATE: 19911011 CLASSIFICATION: 514
                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
                                                                                                  TELEFAX: (703
TELEX: 899149
                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                         CITY: Alexandria
STATE: Virginia
             ORGANISM:
                                                                                                                                                                                                                                                                                               ADDRESSEE:
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10 BP; 369 A; 313
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               Homo sapiens
Monocyte
U937
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                                                                                                                                                             UMBER: PCT/AU90/00603
20-DEC-1990
                                              cDNA to mRNA
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Pred. No. 3.96e+02
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                                                                                                                                                                                                                                                                                                                                                                                           BP.
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RESULT 182
ID US-08-466-337A-17 STANDARD; DNA; UNC; 1550
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Best Local Similarity 100.0%;
Matches 9; Conservative
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OTHER INFORMATION: /note= "Codes for human plasminogen activator
OTHER INFORMATION: inhibitor type 2 protein in which amino acids
OTHER INFORMATION: to 96 inclusive have been deleted."
SEQUENCE 1512 BP; 449 A; 318 C; 324 G; 421 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/08466337A Sequence 17, Application US/08466337A Patent No. 5830756
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TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/466,337A FILING DATE: 06-UN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haskill, John S.
APPLICANT: Baldwin Jr., Albert S.
APPLICANT: Ralph, Peter
TITLE OF INVENTION: Inhibitor of NF-kB Transcriptional
TITLE OF INVENTION: Activator and Uses Thereof
                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 32,167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-6400
                                             FEATURE:
                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION: /fur
OTHER INFORMATION: /pr
OTHER INFORMATION: /pr
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OTHER INFORMATION: /ew
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CLONE: BTA 1916
    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                              NAME: Pochopien, Donald REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300
CITY: Chicago
                                                                                        TOPOLOGY:
                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                           LENGTH:
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                                                                                                                                             1550 base pairs
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                                                                                     linear
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                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function- "Product binds to urokinase, tissue plasminogen activator" /product- "PAI-2 variant, protease sensiremoved"
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Pred. No. 3.96e+02;
0; Mismatches of
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Query Match Best Local S Matches

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APPLICANT:

ADDRESSEE:

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Query Match 100.0%;
Best Local Similarity 100.0%;
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LOCATION: 95
SEQUENCE 1550 BP;
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          JT 184
US-08-252-995D-5 STANDARD; DNA; UNC; 1600 BP.
                                                                                      1261 TTCTGAGAA 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08475359
Sequence 17, Application US/08475359
Patent No. 5846714
GENERAL INFORMATION:
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US-08-475-359-17 STANDARD; DNA; UNC; 1550
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                              25 ttctgagaa 33
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                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/475,359
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Inhibitor of NF-kB Transcriptional TITLE OF INVENTION: Activator and Uses Thereof NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                 TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1550 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baldwin Jr., Albert S
APPLICANT: Ralph, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     NAME: Pochopien, Donald J. REGISTRATION NUMBER: 32,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 S
                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States ZIP: 60606-6402
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Similarity 100.0%;
9; Conservative
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                                                                                                                Conservative
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95.1045
P; 380 A; 402 C; 416 G; 352 T; 0 OTHER.
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Pred. No.
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Pred. No. 3.96e+02
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South Wacker Drive
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Best Local Similarity 100.0%;
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REFERENCE/DOCKET NUMBER: 3153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEPAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 206..1597
SEQUENCE 1600 BP; 482 A;
                         Sequence 1, Application Sequence 1, Application Patent No. 5444153 GENERAL INFORMATION:
                                                                                                  T 185
US-07-768-286B-1 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08252995D Sequence 5, Application US/08252995D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopov 3'
COMPUTED
                                                                                                                                                                              527 TTCTCAGAA 535
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                                                                                                                                                                                                                                                                              LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Kurdydyk, Linda M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 02-JUN CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Lymphoid cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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GOSS, Neil H. RICHARDSON, M
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                                                  US/07768286B
US/07768286B
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                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 49.1296
OTHER INFORMATION: /
OTHER INFORMATION: a
SEQUENCE 1610 BP; 485 A; 3
                    Sequence 4, Application Sequence 4, Application Patent No. 5792903 GENERAL INFORMATION:
                                                                               л 186
US-08-399-561-4 STANDARD;
                                                                                                                                   1016 TTCTGAGAA 1024
                                                                       XXXXXX
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/AU90/00603
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/157 C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)838-4109
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pair
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Local Similarity 100.0%;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
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CLONE: BTA 1445
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  APPLICANT:
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
CELL TYPE: Monocyte
CELL LINE: U937
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CITY: Alexandria
STATE: Virginia
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FILING DATE: 19911011
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 Hirschberg, Joseph
Cunningham Jr., Fr
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Pred. No. 3.96e+02;
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Sequence 2, Application U
Patent No. 5831055
GENERAL INFORMATION:
APPLICANT: BIENKOWSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 810-539-5055
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1614 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                   XXXXXX
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US-08-709-923-2 STANDARD; DNA; UNC; 1625
                                                                                                                                                                                                                                                                                                                              1224 TTCTGAGAA 1232
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TISSUE TYPE: Leaf
SEQUENCE 1614 BP; 447 A; 288 C; 370 G; 509 T; 0 OTHER.
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Local Similarity 100.0%;
tes 9; Conservative
        COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
                                                                                                                                                      APPLICANT: BIENKOWSKI, MICHAEL J.
TITLE OF INVENTION: NOVEL KIDNEY
TITLE OF INVENTION: CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 810-539-5050
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NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gantt, Elisabeth
TITLE OF INVENTION: Lycopene Cyclase Gene
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5792903thwestern Highway, Suite
CITY: Farmington Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US
  CURRENT APPLICATION DATA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                   COUNTRY: UZIP: 49001
                                                                                         STATE:
                                                                                                             STREET:
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US/08709923
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Pred. No.
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Sequence 1, Application US/08460895
Patent No. 5849508
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                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/650, 805
FILING DATE: 06-FEB-1991
APPLICATION NUMBER: FR8001596
FILING DATE: 12-FEB-1990
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 616-833-009/
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1678 hase pair
                                                                                                                                                                                                                                                                                                                                                                   GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 ttctgagaa 33
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 500 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: MS-DOS version 3.0 or above
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,895
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 100.0%; Local Similarity 100.0%; es 9; Conservative
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REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-7914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Wootton, Thomas A.
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        APPLICANT: BRECHOT, Christian
APPLICANT: WANG, Jian
APPLICANT: CHENIDESEE, Xavier
APPLICANT: HENGLEIN, Berthold
                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                         APPLICANT: HENGLEIN, Berthold
APPLICANT: ZIMDY, Fr d rique
TITLE OF INVENTION: NEW HUMAN CYCLIN A COMPOSITIONS AND A PROCESS FOR THEIR
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: N-terminal UENCE 1625 BP; 444 A; 399 C;
                                                                                                                                                                                                                                    ADDRESSEE: Larso
STREET: 727 Twen
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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TOPOLOGY: li
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                             LENGTH:
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                  nucleic acid
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EDNESS: single
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                             1634 base pairs
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linear
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         single
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Patent No. 5449756

Patent No. 5449756

APPLICANT: TANIGUCHI, TADATSUGU; HATAKEYAMA, MASANORI; MINAMOTO, SEJIRO; KONO, TAKESHI; DOI, TAKESHI; MIYASAKA, MASAYUKI; TSUDO, MITSURU; KARASUYAMA, HAJIME
TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSUDO, MITSURU; KARASUYMA, HAJIME
TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5198359.

Patent No. 5198359

APPLICANT: TANIGUCHI, TANATSUGU; JATAKEYAMA, MASANORI;

MINAMOTO, SEJIRO; KONO, TAKESHI; DOI, TAKESHI; MIYASAKA, MASAYUKI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:9:
                                                                                          SEQ ID NO:9:
                                                                     LENGTH: 1656
Sequence 1794 BP;
                                                                                                                                                                                                                                                                                    01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1653
Sequence 1791 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: coding sequence from base 97 to base 1392, LOCATION: coding for a protein of 432 amino acids. SEQUENCE 1634 BP; 475 A; 354 C; 376 G; 429 T; 0 OTHER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                 279
 282 TTCTCAGAA 290
                                                                                                     APPLICATION NUMBER: US/08/88
FILING DATE: 9-JUL-19-3
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 865,155
FILING DATE: 08-APR-1992
APPLICATION NUMBER: 487,059
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       968 TICTGAGAA 976
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APPLICATION NUMBER: US
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                 TTCTCAGAA 287
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                      h 100.0%;
Similarity 100.0%;
9; Conservative
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Similarity 100.0%;
9; Conservative
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Similarity 100.0%;
9; Conservative
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                                                                     317 A; 559 C; 456 G; 324 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      560 C;
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                                                                                                                                                                            us/08/88,592
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Pred. No.
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Pred. No.
                                 Score 9; DB 5; L
Pred. No. 3.96e+02
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3.96e+02;
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                                             Length 1656
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                                                                     138 other;
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RESULT 191
ID 5198359-5 STANDARD;
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5198359.
Patent No. 5198359
Patent No. 5198359
APPLICANT: TANIGUCHI, TADATSUGU;JATAKEYAMA, MASANORI;
APPLICANT: TANIGUCHI, TAKESHI;DOI, TAKESHI;MIYASAKA, MASAYUKI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 504, ...
Parenal INFORMATION:
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Sequence 1794 BP; 317 A; 560 C; 456 G; 323 T; 138 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08476008
Sequence 4, Application US/08476008
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                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/306,063

FILING DATE: 13-SEP-1994

APPLICATION NUMBER: US 07/749,611

FILING DATE: 28-AUG-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXXXX
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Local Similarity 100.0%;
hes 9; Conservative
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                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
PADICOCATION MADER. US COS 1/15 COS
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
 ATTORNEY/AGENT INFORMATION:
          APPLICATION NUMBER: US 0 FILING DATE: 31-AUG-1990 CLASSIFICATION: 435
                                                                                                                                               APPLICATION NUMBER: US/08/476,008 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                               STREET: 700 Ches
CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/487,059 FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                     Missouri
                                                                                                                                                                                                                                                                                                                             E: Dennis R. Hoerner, Jr., Monsanto Co. 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                        USA
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                                        US 07/576,537
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Pred. No. 3.96e-
0; Mismatches
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ID US-08-833-485-4 STANDARD; DNA; UNC; 1673
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LOCATION: 86..1432
SEQUENCE 1673 BP; 354 A; 517 C; 485 G; 317 T; 0
                                APPLICATION UNMER: US/08/833,485
FILING DATE: 07-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION UNMER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
PRIOR APPLICATION UNMER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
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INFORMATION FOR SEQ ID NO: 4:
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Local Similarity 100.0%;
les 9; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsa
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
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FEATURE:
            ATTORNEY/AGENT INFORMATION: NAME: Hoerner Jr., Denni
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                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: . 1673 base pairs TYPE: nucleic acid STRANDEDNESS: double
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 REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         Missouri
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, Dennis R.
R: 30,914
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US/08833485
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Pred. No. 3.96e+02
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Best Local Similarity 100.0%;
Matches 9; Conservative
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LOCATION: 86..1432
SEQUENCE 1673 BP; 354 A; 517
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Sequence 4, Application US/08306063
Patent No. 5633435
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SEQUENCE CHARACTERISTICS:
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 ttctgagaa 33
                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                  APPLICATION NUMBER: 0
FILING DATE: 13-SEP-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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TELECOMMUNICATION INFORMATION:
                                 REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 28-AUG-1991 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                  NAME: Hoerner Jr., Dennis R. REGISTRATION NUMBER: 30,914
                                                                                                               APPLICATION NUMBER: US 07/576,537 FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (314)737-6099
(314)737-6047
                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Barry, Gerard F.
Kishore, Ganesh M.
                      (314)537-6047
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N: 435
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Pred. No.
0; Misma
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                                                                                                                                                                                                                                             Version #1.25
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Best Local Similarity 100.0%;
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                                                                 1653 TTCTGAGAA 1661
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LOCATION: 86..1432
SEQUENCE 1673 BP; 354 A;
LOCATION: 86..1432
SEQUENCE 1673 BP; 354 A; 517 C; 485 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
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PCT-US91-06148A-4 STANDARD; DNA; UNC; 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US91/0614
FILING DATE: 19910828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 ttctgagaa 33
                                                                                                        REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEPHAX: (314)537-6047
                                                                                                                                                                                             APPLICATION NUMBER: US/O FILING DATE: 28-AUG-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                 APPLICATION NUMBER: US 0
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          PRIOR APPLICATION: 800
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 36
                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                      MOLECULE TYPE:
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TYPE: n
          NAME/KEY:
                                                STRANDEDNESS: do TOPOLOGY: linear
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TOPOLOGY: 11
                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                   CDS
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                                      DNA (genomic)
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 317 T; 0 OTHER
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Best Local
                                         1491 TTCTCAGAA 1499
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LOCATION: 1..1698
SEQUENCE 1701 BP; 392 A; 470 C; 421 G;
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US-08-484-993B-40
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Sequence 40,
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INFORMATION FOR SEQ ID NO:
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                                                                              Match 100.0%;
Local Similarity 100.0%;
nes 9; Conservative
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REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1701 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/484,993B FILING DATE: 09-NOV-1993 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/012,990 FILING DATE: 29-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                        MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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APPLICANT: HSu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception
                            ttctcagaa 25
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Similarity 100.0%;
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Application US/08484993B
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Tower, 233
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Pred.
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Pred. No. 3.96e+02
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3.96e+02;
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ID US-08-247-809A-5 STANDARD; DNA; UNC; 1722
AC XXXXX
DT
DE Sequence 5, Application US/08247809A
CC Sequence 5, Application US/08247809A
CC Patent No. 5569823
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Best Local Similarity 100.0%;
Matches 9; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1722 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 475..1428
SEQUENCE 1722 BP; 580 A;
                                                                              Sequence 17, Application Sequence 17, Application
                                                                                                                       XXXXXX
                                                                                                                                  US-08-417-330A-17 STANDARD; DNA; UNC; 1732
                                                     Patent No. 5719057
GENERAL INFORMATION:
                                                                                                                                                                                                   984 TTCTGAGAA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READMAILE FORM:
MEDIUM TYPE: Diskette, 3
MEDIUM TYPE: storage
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TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
                            APPLICANT:
                                          APPLICANT:
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APPLICATION NUMBER: P 43 :
FILING DATE: May 28, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peter H. Schreier; Klaus Stenzel; Gunter Adam;
Edgar Maiss
LE BOURDELLES, BEATRICE WHITING, PAUL WINGROVE, PETER
                                          HADINGHAM, KAREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEC Powermate 1 Plus
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US/08417330A
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Pred. No.
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF COXIELLA BURNETII IN BIOLOGICAL FLUIDS
   SEQ
                                                                                                                                                                   Patent No. 525828
Patent No. 5258283
                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence
LOCATION: 27...1385
OTHER INFORMATION:
SEQUENCE 1732 BP; 508 A; 366 C; 354 G;
                                                                                                                                                                                                                                                                                         1477 TTCTCAGAA 1485
                                                                                                                                                                                                                    5258283-8 STANDARD; DNA; UNC; 1894 BP
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                                                                                                                                                                                                                                                                 33 ttctcagaa 25
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SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,330A
FILING DATE: 05-APR-1995
                                                           APPLICATION NUMBER: US/
FILING DATE: 23-OCT-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: T1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                              NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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NAME: HAND, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA
APPLICATION NUMBER: 927,779
FILING DATE: 05-NOV-1986
APPLICATION NUMBER: 795,207
FILING DATE: 05-NOV-1985
) NO:8:
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126 EAST LINCOLN AVENUE - P.O.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XXXXXX
                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Pattea L.
REGISTRATION UNMER: 31,284
REFERENCE/DOCKET NUMBER: MGS1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/453,84
FILING DATE: 30 MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,607
FILING DATE: 13-SEPT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                807 TTCTCAGAA 815
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                                                  FEATURE
                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
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HYPOTHETICAL: N
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STREET:
CITY: At
                         NAME/KEY:
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  coding region for AcNPV 61K protein signal
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Query Match
Best Local Similarity 100.0%; LENGTH: 1749 Sequence 1894 BP; Conservative 579 A; 335 C; 343 G; 492 T; 145 other; Pred. Score 0 Mismatches 9; DB 5; Le No. 3.96e+02; Length 1749 Indels 0 Gaps

0

T 200 US-08-453-848-14 STANDARD; DNA; UNC; 1757 BP. US/08453848 US/08453848

CORRESPONDENCE ADDRESS: TITLE OF INVENTION: E: Patrea L. Pabst 2800 One Atlantic Center 1201 West Peachtree Stre Volvovitz, Franklin Wilkinson, Bethanie Hackett, Voznesensky, Andrei Smith, Gale Eugene Craig Stanway
A METHOD FOR PRODUCING INFLUENZA HEMAGGLUTININ MULTIVALENT VACCINES Eident

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA: Release #1.0, Version

US/08/453,848

MGS101CIP

INFORMATION FOR SEO ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid INDIVIDUAL ISOLATE: linear Influenza virus single DNA (genomic) A/Shandong/9/93 rHA 14:

IRESULTION IN COLUMN IN CO

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polyhedrin mRNA leader (partial) 1 to 18

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CC LOCATION: 19 to 72
CC FEATURE:
CC NAME/KEY: Smal restriction site
CC LOCATION: 76 to 81
CC FEATURE:
CC NAME/KEY: coding region for mature rHA
CC LOCATION: 73 to 1728
CC FATURE:
CC NAME/KEY: KpnI restriction site
CC FEATURE:
CC NAME/KEY: BglII restriction site
CC FEATURE:
CC NAME/KEY: BglII restriction site
CC FEATURE:
CC NAME/KEY: BglII restriction site
CC FEATURE:
CC NAME/KEY: Universal translation termination signal
CC LOCATION: 1741 to 1746
CC FEATURE:
CC NAME/KEY: Universal translation termination signal
CC LOCATION: 1747 to 1757
SQ SEQUENCE 1757 BP: 582 A: 352 C: 403 G: 420 T: 0 OTHER.

Query Match
Destruction of the complete of the conservative of Mismatches of Indels of Gaps of Matches of Tottcagaa 25

Db 1276 TTCTCAGaa 25
Search completed: Thu Oct 28 00:34:43 1999

Job time: 59 secs.
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Result C	Statistics: Me Pred. No. is score greater and is derive	Database:	Database:	Searched: Post-processing:	Nmatch STD:	Scoring table:	Title: Description: Perfect Score: N.A. Sequence: Comp:	Run on: Tabular output r	Release 3 Copyright Di		********
100.0 63 18 AA794827 Vr48a09.S1 Knowles Sol 2.23e+03 70 13 AAA72837 Vd58f06.r1 Knowles Sol 2.23e+03 100.0 114 21 AA4974588 op28h09.S1 Soares.NFL 2.23e+03 100.0 119 16 AA623551 Vn72e08.r1 Knowles Sol 2.23e+03 100.0 124 16 AA62562 nr16g04.s1 NCI_CGAP_Ew 2.23e+03 100.0 130 14 AA509777 Vh52e10.r1 Soares mous 2.23e+03 100.0 140 9 AAA204121 mu57d04.r1 Soares mous 2.23e+03 100.0 142 16 AA628553 af39a11.s1 Soares.tota 2.23e+03 100.0 145 10 AA229563 nc15e08.s1 NCI_CGAP_Pr 2.23e+03 100.0 149 12 AA386233 EST07409 Hippocampus H 2.23e+03 100.0 149 12 AA386233	! !	Mean 5.524; Variance 0.786; scale 7.024 o. is the number of results predicted by chance to have a reater than or equal to the score of the result being printed, derived by analysis of the total score distribution.	ank-est111 ank-est111 gb_est1 9:gb_est15 15:gb_est1 :gb_est18 18:gb_est15 19:gb_est2 :gb_est18 18:gb_est19 19:gb_est2 :gb_est21 22:gb_est2 23:gb_est2 :gb_est25 26:gb_est26 27:gb_est2 :gb_est25 26:gb_est3 31:gb_est4 :gb_est7 35:gb_est8 36:gb_est9 :gb_est7 35:gb_est8 36:gb_est9 :gb_est8 40:gb_gss4 41:gb_gss5	t58 est10 2:em_	2883791 seqs, 1171580779 bases x 2 : Minimum Match 100% Listing first 200 summaries	; Query 0	TABLE default Gap 6	>US-08-963-288-1 (25-33) from US08963288.seq 9 25 ttctgagaa 33 aagactctt	Thu Oct 28 00:25:53 1999; MasPar time 79.16 Seconds 266.410 Million cell updates/sec not generated.	se 3.1A John F. Collins, Biocomputing Research Unit. ight (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd n.a. database search, using Smith-Waterman algorithm		***************************************
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EST47561 Fetal spleen EST02957 Mouse 7.5 dpc vt81d04.r1 Barstead mo nk96d07.s1 NCI_CGAP_Co RICS12347A Rice green EST23709 Human Bone Ho vs52c12.r1 Stratagene vn12h05.r1 Stratagene nk47h12.s1 NCI_CGAP_GC EST49984 Gall bladder	EST94617 Fetal brain I EST94617 Supt cells Ho HSCOCE011 normalized i EST79569 Human Placent zx72f1i.rl Soares_tota	32546 Lambda-PRL2 Arab nq49904.s1 NCI_CGAP_Co EST95699 Testis I Homo nm07d03.s1 NCI_CGAP_Co zr53f07.s1 Soares_NhHM	np2hi0.si NCI_CGAP_GC ve46h02.rl Soares mous EST79880 Placenta I Ho EST15028 Aorta endothe EST201407 Normalized r nf18a04.si NCI_CGAP_Br os64f02.si NCI_CGAP_Br op56903.si NCI_CGAP_T np190h01.si NCI_CGAP_T np190h01.si NCI_CGAP_Th	al59a06.sl Soares_NFL_vx20el1.rl Soares 2NbM A275F Heart Homo sapie	mv58d03.rl Soares mous zs11f10.rl NCI_CGAP_GC zv51h05.rl Soares_test HSC2TA072 normalized i	EST66720 Fetal lung II CT093.UNI Tomato Leaf nt02b09.sl NCI_CGAP_Ly	mg88f02.rl Stratagene c HSDHE0117 Stratagene c vs39c12.rl Stratagene	v14/c10.51 Stratagene nk55h06.s1 NCI_CGAP_Pr D43291 Rice callus cDN hbc032B Human pancreat vk64b02.r1 Stratagene	EST14416 Testis tumor oc29e10.sl NCI_CGAP_GC EST95014 Activated T-c EST78389 Pancreas tumo ucananawa u uman adu	zs46c05.1 NOI_CGAP_GC vk69e10.sl Knowles Sol TBNU1182 T. cruzi epim. aa95e01.rl Stratagene ok61f05.sl NCI_CGAP_GC	m5g16a1.Tl Aspergillus EST190888 Normalized r mt73f01.11 Soares mous zh40b06.sl Soares_pine mu80a11.rl Stratagene EST80794 Placenta II H vm31g02.rl Knowles Sol zr96h04.rl NCI_CGAP_GC EST15175 Aorta endothe	vs60d02.rl Stratagene vd58f07.rl Knowles Sol CS14AX Chinook salmon
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REFERENCE
AUTHORS
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Eukharjota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 70)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuqi
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. LC Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA472837 70 bp mRNA EST 18-JUN-1997 vd58f06.rl Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:804803 5' similar to TR:E128396 E128396 XPMC2 PROTEIN.
                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:692466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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                                          Trace considered overall poor quality possible reversed clone: similarity or
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forest Park Parkway, Box 8501, St. 314 286 1800
quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1123864"
/clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
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/strain="B6D2 F1/J"
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JOURNAL COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 491 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:692499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        op28h09.sl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578209 3', mRNA sequence.
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Similarity 100.0%;
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/notes "Organ: pooled; Vector: pT773D-Pac (Pharmacia) with /notes "Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/db_xref="taxon:10090"
/clone="IMAGE:804803"
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Site_2: SalI; Cloned unidirectionally from mRNA prepared
from 800 blastocysts. Primer: SalI(dT):
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/tlssue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
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Best Local Similarity 100.0%;
Matches 9; Conservative
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                              vector to vector length is 389
High quality sequence stop: 106
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:577534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lk
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On Apr 14, 1993 th
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/lab_host="DH10B"
27 c 21 g 36 t
                                                                                           /clone_lib="Knowles Solter mouse blastocyst Bl"
/tlssue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
25 c 20 g 38 t
                                                                                                                                                                                        inserts) and B3."
/db_xref="taxon:10090"
/clone="IMAGE:1037510"
                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain=".B6D2 F1/J"
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Score 9;
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similar to
                                  AA509777 130 bp mRNA EST 08-JUL-1997 vh52e10:r1 Soares mouse mammary gland NbMG Mus musculus cDNA IMAGE:890634 5' similar to gb:L20450 Mus musculus DNA-binding protein mRNA, complete cds (MOUSE);, mRNA sequence.

AA509777
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Location/Qualifiers
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Unpublished (1997)
On Sep 12, 1996 th
92247631
AA509777.1
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Similarity 100.0%;
9; Conservative
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Email: Robert_Strausberg@nih.gov
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National Cancer Institute, Cancer Genome Anatomy
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AA662562.1
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/note="Vector: pAMP10; mRNA made from Ewing's sarcoma,
/note Vector: pAMP10; mRNA made from Ewing's sarcoma,
cDNA made by oligo-dT priming. Non-directionally clor
Size-selected on agarose gel, average insert size 600
Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
30 c 18 g 52 t
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1168182"
/clone_lib="NCI_CGAP_Ewl"
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2.23e+03;
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Local Similarity 100.0%;
les 9; Conservative
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                                                                                                                           AA204121 140 bp mRNA EST 27-JAN-1997 mu57d04.rl Soares mouse lymph node NbMLN Mus musculus cDNA climAGE:643495 5' similar to gb:X56548 M.musculus Np-b mRNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 130)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The Washu-HHMI Mouse EST Project
                                                                                          purine-nucleoside phosphorylase
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Mus musculus
                                                                        g1800757
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High quality sequence stop: 1.
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Fax: 314 286 1810
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                                                      AA204121.1
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                   house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
24 c 25 g 40 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares mouse mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:890634"
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                                                                                                                                        AA628553 142 bp mRNA EST 16-OCT-1997 af39a11.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034012 3' similar to WP:W02B12.9 CE03769 MITOCHONDRIAL RN SPLICING MSR4 LIKE PROTEIN ;, mRNA sequence.

AA628553
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 142)
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This clone is available royalty-free through LLNL; contact the
TMACE Consortium (info@image.llnl.gov) for further information.
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On Apr 14, 1993 th
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Similarity 100.0%;
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of MedicineP
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WashU-HHMI Mouse EST Project
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker: Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DHIOB"
28 c 29 g 39
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/strain="C57BL/6J"
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Pred. No. 2.23e+03;
0; Mismatches 0
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Matches 9; Conservative
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                      sequence.
AA229563
                                                                                                                                                                                                                                                                                                                                                     AA229563 145 bp mRNA EST 20-AUG-1997 nc15e08.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008230 similar to gb:L29008 SORBITOL DEHYDROGENASE (HUMAN);, mRNA
                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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42 c 34
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/dev_stage="8-9 weeks"
                                                                       1996 this sequence version replaced g1:1394888
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d. No. 2.23e+03;
Mismatches 0;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 149)

RRS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Fields, C., Fraecr, C., Man, Vanter, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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EST07409 Hippocampus Homo sapiens cDNA 3' e
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Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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//Organism="Homo sapiens"
//note="Vector: pANP10; Site_1: Not1; Site_2: ECORI; lst
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
/clone="MANGE:1008330"
/clone="MANGE:1008330"
/clone="MANGE:1008330"
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/lab_host="DH10B"
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Pred. No. 2.23e+03;
0; Mismatches 0
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 ttctgagaa 33
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96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us60d02.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1150659 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2287244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 150)
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Email: arkerlav@tigr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive,
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA930548.1 GI:3080038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_ESTs:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
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                                                                                                                                                                                  IMAGE Consortium (info@image.linl.gov)
                                                                                                         primer: -28ml3 rev1 ET from
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/organism="homo brain; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: EcoRI"
/db_xref="taxon:9606"
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/tissue_type="hippocampus"
41 c 34 g 32 t
/organism="Mus musculus"
                                                                    Location/Qualifiers
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Pred. No. 2.23e+03;
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JOURNAL
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 151)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA472838 151 bp mRNA EST 18-JUN-1997 vd58f07.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:804805 5' similar to TR:E128396 E128396 XPMC2 PROTEIN; mRNA sequence.
                                                                                                                                                                                Trace considered overall poor quality possible reversed clone: similarity on High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
On Apr 14, 1993 th
                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
The WashU-HHMI Mouse EST Project
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W
                                       /note-"Organ: embryo; Vector: pSPORT; Site_1: NotI; Site_2: SalI; Cloned unidirectionally from mRNA prefrom 800 blastocysts. Primer: SalIdT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTT-3'. cDNAs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cloned into the NotI/SalI sites of a pSPORT vector Technologies). Two different size selections: Bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin
28 c 33 g 50 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1150659"
/clone_lib="Stratagene mouse
/sex="females"
                                                                                                                      /organism="Mus musculus"
/strain="B6D2 F1/J"
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Best Local Similarity 100.0%;
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AA786748 156 bp mRNA EST 31-JUL-1998 m5906a1.rl Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CS14AX chinook salmon
CS14AX 5' end similar
T23127
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 65-8742860
Fax: 65-7792486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Zhiyuan Gong
School of Biological Sciences
National University of Singapore
Lower Kent Ridge Road, Singapore 119260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Atlantic halibut cDNAs 
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Scorpaeniformes; Cottoidei; Cyclopteridae; Cyclopterus.
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Cyclopterus lumpus
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T23127.1 GI:505948
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33
                                                                                                                                                                                                                                                                                                      /organism="Cyclopterus lumpus"
/note="Vector: Lambda Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from several pituitaries of the chinook salmon. cDNA was directly cloned into the lambda ZAPII vector using the Stratagene's Lambda Uni-ZAP XR cD cloning system."
                                                                                                                                                                                                                                                                      cloning system. "
/db_xref="taxon:8103"
/clone="CS14AX"
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/clone_lib="Knowles Solter mouse blastocyst B1"

/tissue_type="blastocyst"

/dev_stage="embryo (pre-implantation)"

/lab_host="DH10B"

34 c 46 g 32 t
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/db_xref="taxon:10090"
/map="959H08; 1"
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19 c 36 g 43 t
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2.23e+03;
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                                                                                                                                           Rattus sp.
Eukaryota;
Eutheria; R
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 159)
Lee, N. H.; Glodek, A.; Chandra, I., Mason, T. M.; Quackenbush, J.; Kerlavage, A. R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Chemistry and Blochemistry
Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
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AA786748
Unpublished (1998)
On Sep 12, 1996 this sequence
Other_ESTs: EST190889
                                                                                                                                                                                                                                                                                                         EST190888 Normalized rat s
RSPAA38 3' end similar to
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Location/Qualifiers
1. .156
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We anticipate the future
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eurotiales: Trichocomaccae: Emericella.

1 (bases 1 to 156)

Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W.,
Prade,R. and Roe,B.

Aspergillus nidulans EST Database
Unpublished (1998)

On Jan 19, 1998 this sequence version replaced gi:2
                                                                                                                                                                                                                                                                         sequence.
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Eukaryota; Fungi; Ascomycota; Euascomycetes; Plectomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library" /tissue_type="vegetative mycelia, asexual structures" /tissue_type="vegetative mycelia, asexual structures" 27 c 38 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5; end of cDNA cloned into EcoRI site of pBluescript
3; end of cDNA cloned into XhoI site of pBluescript"
/db_xref="taxon:5072"
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/strain="FGSC A26"
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o FGF-binding protein
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2.23e+03;
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                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
On Sep 12, 1996 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 160)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA165736 160 bp mRNA mt73f01.rl Soares mouse lymph node NbMLN IMAGE: 635545 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: nhlee@tigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712, Medical Center Drive, Rockville,
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                        MGI:387537
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                    quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                         mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: spleen; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
                                           /organism="Mus musculus"
/strain="C57BL/6J"
/note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco R
1st strand cDNA was primed with a Not I - oligo(dT) prim
/db_xref="ATCC (inhost):2009482"
/db_xref="taxon:10118"
/clone="RSPAA38"
                                   1st strand
[5'
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Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST project Unpublished (1997)
On Nov 6, 1997 this sequence version replaced gi:947573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA719466 162 bp mRNA E: zh40b06.s1 Soares_pineal_gland_N3HPG Homo IMAGE:414515 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
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Seq primer: -40ml3 fwd. ET from Amersham
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                                                                           (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo." /db_xref="texon:10090"
/clone_lib="Soares_pineal_gland_N3HPG"
/lab_host="DH10B (ampicillin resistant)"
33 c 30 g 42 t
                                                               /clone="IMAGE:414515"
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/dev_stage="4 weeks"
/lab_host="DH10B"
39 c 23 g 53
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/sex="male"
                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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No. 2.23e+03
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AA212257
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 164)
1 (bases 1.111.-- , allen M. Bowles, M., Dietrich, N., Dubug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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On Apr 14, 1993 this sequence ver
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AA212257.1
 AA369389
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                                                                                                                                                                                                       52
                                                                                                                                                                                                                                                                                                               /clone_lib="Stratagene mouse melanoma (#937312)"
/tissue_type="melanoma"
/dev_stage="M2 cells"
/lab_host="SOLR (kanamycin resistant)"
41 c 45 g 26 t
                                                                                                                                                                                                                                                                                     /clone="IMAGE:651836"
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

AL Nature 377 (6547 Suppl), 3-174 (1995)
                                                  AA574819 173 bp mRNA EST vm31g02.rl Knowles Solter mouse blastocyst clone IMAGE:991826 5', mRNA sequence AA574819
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                            g2349445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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AA574819.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/note="Organ: placenta; Vector: pl
EcoRI; site_2: XhoI"
/db_xref="ATCC (inhost):174008"
/db_xref="taxon:9606"
/clone_lib="placenta II"
/tissue_type="placenta"
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GI:2349445
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                                                                                                                           Mus musculus cDNA
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                     28 TTCTCAGAA 36
                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 173)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                   AA415399 173 bp mRNA EST 13-AUG-1997
Zr96h04.r1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:683575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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The WashU-HHMI Mouse EST Project
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                         mRNA sequence.
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Similarity 100.0%;
9; Conservative
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inserts) and B3."
/db_xref="taxon:10090"
/clone="IMAGE:991826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Knowles Solter mouse blastocyst B1"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="B6D2 F1/J"
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RESULT 22
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Best Local Similarity 100.0%;
Matches 9; Conservative
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1 (bases 1 to 176)

12 1 (bases 1 to 176)

13 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

14 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,

15 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,

16 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,

17 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,

18 Glodek,A., Glehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,

19 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,

19 Glodek,A., Glehm,C.L., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

19 Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

20 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

21 Small,R.V., Sprigys,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

22 Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

23 Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,

24 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,

25 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Ruben,S.M.,

26 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
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AA302027.1 GI:1954420
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Email: Robert_Strausberg@nih.gov
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Eutheria; Primates;
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Location/Qualifiers
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Tel: (301) 496-1550
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/lab_host-"DH10B"
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/clone_lib="NCI_CGAP_GCB1"
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5841 S. Maryland Ave.,MC1028,Chicago
Tel: 3127029116
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T18548.1
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 178)

Bell,G.I. and Takeda,J.

Human pancreatic islet cDNAs

Unpublished (1995)

On Sep 21, 1992 this sequence version replaced g1:276270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96026280
On Sep 12, 1996 this sequence version replaced gi:1407137 Other_ESTs: THC190585
                                                                                                                                 Email: g-bell@uchicago.edu
                                                                                                                                                    Fax: 3127020271
                                                                                                                                                                                                                                       Contact: Bell GI or Takeda J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bioinformatics
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho I; mRNA was prepared from normal adult human islets. cDNA was directionally synthesized from the Xho I in the vector to the EcoRI site. cDNA was size fractionated to remove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_llb="Aorta endothelial cells"
/cell_type="endothelial cell"
/dev_stage="adult"
/dev_stage="adult" 38 t 2 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: aorta; Vector: pBluescript
EcoRI; Site_2: XhoI"
/db_xref-"ATCC (inhost):114253"
/db_xref-"taxon:9606"
                                                                  /organism="Homo sapiens"
                                                                                                Location/Qualifiers
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Query Match 100.0%;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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/db_xref="taxon:9806"
/clone="hbc2035"
/clone_lib="Human pancreatic
1 26 c 30 g 66 t
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No. 2.23e+03;
    DB 10; Length 184; 2.23e+03;
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185 bp mRNA

VR69e30.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone

IMAGE:959946 5' similar to gb:M88163 POSSIBLE GLOBAL TRANSCRIPTION

ACTIVATOR SNF2L (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:548738
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
Wash'-HMI Mouse EST Project
Wash's HMI 
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 185)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: embryo; Vector: pBluescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(dT): 5'-CGGTCGACCGTTTTTTTTTTTTTTTT-3'
were cloned into the MluI/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
/clone="IMAGE:959946"
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Knowles Solter mouse 2
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
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/strain="B6D2 F1/J"
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187 bp mrNA EST 07-JUL-1998 cruzi epimastigote normalized cDNA Library Trypanosoma
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                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 187)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,Strizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Washd-NCI human EST project Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1392955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Medical Genetics Uppsala University Biomedical Center, Box 589, S-751 Tel: 46 18 471 45 85 Fax: 46 18 52 68 49
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1 (Dases 1 to 187)

Porcel,B., Tran,A-N., Andersson,B., Nyarady,Z., Urmenyi,T.P., Rondinelli,E., Pettersson,U. and Aslund,L.

Generation of Expressed Sequence Tags from Trypanosoma cruzi Unpublished (1998)

On Sep 1, 1995 this sequence version replaced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
AA488722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aa95e01.r1 Stratagene fetal retina 937202 Homo
IMAGE:839064 5' similar to contains L1.t1 L1 re
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Seq primer: M13 forward
High quality sequence stop: 187
                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA488722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypanosoma cruzi
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AI046096
                    Washington
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     human .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 100.0%;
Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Aslund L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma cruzi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Trypanosoma cruzi"
/strain="C1-Brenner"
/note="CNA library constructed with oligo dT primed epimastigote mRNA and cloned in pt7t318D phagemid with modified polylinker (PHARMACIA)"
/db_xref="taxon:5693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="T. cruzi epimastigote normalized
/cell_type="epimastigote"
59 c 40 g 55 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="20f19"
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                    University
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                    of Medicine
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2.23e+03;
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no sapiens cDNA clo

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JOURNAL COMMENT
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ORGANISM
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1736 Std Error: 0.00
Seq priner: -28m13 rev1 ET from Amersham
High quality sequence stop: 144.
Location/Qualifiers
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AA911029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA911029 197 bp mRNA EST 13-APR-1998 ok61f05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518465 similar to TR:Q16342 Q16342 PDCD2-PROGRAMMED CELL DEATH-2/RP8 HOMOLOG. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                               Tel: (301) 496-1550
Email: Robert Charles
                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2284616
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                 Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 167.
                                                                                                                                                                         CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 poole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="SOLR (kanamycin resistant)"
34 c 29 g 51 t
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/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:839064"
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was prepared
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kin, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
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EST14416
AA301402
                                                                                                                                                                                                                9712 Medical Center Drive,
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 197)
                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human index (http://www.tigr.org/tdb/hgi/hgi/html)
                                                                                                                                                                                                                                                                                                                                          Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                       Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                           On Sep 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96026280
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                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
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/clone="IMAGE:518465"
/clone_11b="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
54 c 49 g 51 t
                                Location/Qualifiers
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0; Mismatches 0
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/organism="Homo sapiens"

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RESULT 30 LOCUS DEFINITION
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AUTHORS
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g2876437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allm
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AABU05861 198 bp mRNA EST 25-MAR-1998 core-est NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351146 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Jan 19, 1998 this sequence version replaced gi:2150271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                              /ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                            insert Length: 829
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                                                                                                                                                                                                                                                                                                                        primer: -40m13 fwd. ET from Amersham
quality sequence stop: 183.
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/organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cI polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cI was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: testis; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):191527"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Testis tumor"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               David Allman
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock, K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,R.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Mcorak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wel,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive,
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA381661 199 bp mRNA EST
EST95014 Activated T-cells I Homo sapiens cDNA 5'
similar to protein kinase PKN2, mRNA sequence.
AA381661
                                                                                                                                                                                                                                                            Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                For clone availability, additional sequence and endinformation related to this EST, please check the Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Sep 12, 1996 this sequence version replaced gi:1406865.
Other_ESTs: THC100111
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D.,
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                                                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
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/lab_host="DH10B"
42 c 43 g 51 t
                    /cell_type="T-lymphocyte"
/dev_stage="adult"
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                                                                    /clone_lib="Activated T-cells I"
                                                                                          'db_xref-"taxon:9606"
                                                                                                                 'db_xref="ATCC (inhost):186260"
                                                                                                                                                              note "Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                        organism="Homo sapiens"
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Best Local Similarity 100.0%;
Matches 9; Conservative
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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On Sep 1:
                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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1 (bases 1 to 199)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
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her_ESTs: THC177896
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                                                                                                                                                                                                /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
ECORI; PATCC (Inhost):172019"
/db_xref="taxon:9606"
                                                                                                                        /clone_lib="Pancreas tumor III"
/dev_stage="adult"
33 c 24 g 81 t
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IMAGE:975378 3' similar to SW:RL11_HUMAN P39026
PROTEIN L11. ;, mRNA sequence.
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1 (bases 1 to 203)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuqu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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MRC Human Genome Mapping Project Resource Centre.
The UK-HGMP cDNA program
Unpublished (1993)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                      Waterston, R.
The WashU-HHMI Mouse EST Project Unpublished (1996)
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Clinical Research Centre
Watford Road, Harrow, Middlesex HAl
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: gtll; clone_library=H, Human adult Cortex tissue; cloning vector is gtll. "
/clone_rearraxon:9606"
/clone_lib="H, Human adult Brain Cortex tissue"
/s 53 c 42 g 44 t 1 others
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                                                  Seq
                                                                                                    Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Forman, Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                            Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                     ww-bio.llnl.gov/bbrp/image/image.html
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  clone is available royalty-free through LLNL;
E Consortium (info@image.llnl.gov) for further;
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/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin 39 c 50 g 34 t
/organism="Homo sapiens"
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/strain="C57BL/6"
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Fax: 03-3812-2910
                                                                                                                                                                                                                                                                                                                                                                                                       The University of Tokyo
1-1-1 Yayoi, Bunkyo-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Hirofumi Uchimiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Apr 14, 1993 this sequence version replaced gi:716479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On nucleotide sequence of Oryza sativa Unpublished (1994)
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                                                                                                                                                                                                                                                                                                                                                         huchimiy@tansei.cc.u-tokyo.ac.jp
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                                                                                                                                                                                                  /clone_lib="Rice callus cDNA (H.Uchimiya)"
/tissue_type="callus"
45 c 43 g 61 t 6 others
                                                                                                                                                                                                                                         /...ap="888E02; 6; 6q14.1-6q16.1"
/clone="SS187"
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/lab_host="DH10B"
44 c 32 g 61 t
                                                                                                                                                                                                                                                                              organism="Oryza sativa"
/db_xref="taxon:4530"
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2.23e+03;
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                                               The WashU-HHMI Mouse EST Project Unpublished (1996)
On Sep 21, 1992 this sequence ve
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AA546389
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3'end, m
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Euthesia; Rodentia; Sciurognathi; Muridae; Murinae;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Contact: Marra M/Mouse EST Project washU-HHMI Mouse EST Project
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 205)
Takeda,J., Yano,H., Eng,S., Zeng,Y. and Bell,G.I.
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primer: T7 primer.
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/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
/db_xref="taxon:9606"
/clone="hbc032B"
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AA146148 208 bp mRNA EST 11-FEB-1997 mq88f02.x1 Stratagene mouse melanoma (#937312) Mus musculus cDN/clone IMAGE:585819 5' similar to gb:D10049 Mouse mRNA for mouse melanoma antigen, complete cds (MOUSE);, mRNA sequence.

AA146148
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1 (bases 1 to 208)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                      Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lc Tel: 314 286 1800

Fax: 314 286 1810
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
Seq primer: -28m13 rev1 ET from
High quality sequence stop: 1.
Location/Qualifiers
                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
MGI:360467
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On Sep 12, 1996 this sequence version replaced gi:1395424
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tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
49 c 54 g 29 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genzentrum Muenchen
Laboratorium fuer molekulare Biologie
Am Klopferspitz 18a,8033 Martinsried,Germany
Email: obermaier@vms.biochem.mpg.de
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cat#936208"
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/clone="HE0117"
                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/note="Vector: pBluescript SK(+); Human heart cDNA
library. Cloning vector pBluescript SK(+)"
/db_xref="GDB:D057230E"
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/tissue_type="melanoma"
/dev_stage="M2_cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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0; Mismatches (
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 17; 1998 this sequence version
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Marca, M., Hillier, L., Allen, M., Bowles, M., Dietrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.linl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                            Fetal lung
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/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
50 c 56 g 29 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1148662"
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Pred. No. 2.23e+03;
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                                                          Contact: Ganal, M.W.
Dept. of Cytogenetics
Institute of Plant Genetics and Crop
Corrensstr. 3, D-06466 Gatersleben, G
Tel: 49-39482-5346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA824791
g2897269
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1 (bases 1 to 210)

Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library Nature Genet. 4, 373-380 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Sep 12, 1996 this sequence version replaced gi:1397416.
Other_ESTs: THC101658
Contact: Kerlavage, AR
                                                                                                                                                                              Unpublished (1998)
On Apr 14, 1993 th
                                                                                                                                                                                                                   Sequencing of cDNA clones from the genetic map of (Lycopersicum esculentum)
                                                                                                                                                                                                                                                                                1 (bases 1 to 210)
Ganal, M.W., Czihal, R., Hannappel, U., Kloos, D.-U.,
                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA824791 210 bp mRNA ES7
CT093.UNI Tomato Leaf cDNA from cv. VFNT cl
esculentum cDNA clone CT093, mRNA sequence.
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Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
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                                           Fax: 49-39482-5137
                                                                                                                                                                                                                                                                                                                                                                                                                         tomato.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 3018699423
                                                                                                                                                                                  Apr 14, 1993 this sequence version
il: ganal@mendel.ipk-gatersleben.de
primer: M13-20.
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ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):162236"
/db_xref="faxon:9606"
/clone_lib="Petal lung III"
/dev_stage="fetus"
31 c 45 g 51 t 1 others
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nt02b09.s1 NCI_CGAP_Lym3 Homo
similar to TR:G189397 G189397
                                                                                                                                                                                                         Insert Length: 648 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should kept in mind should you use this clone.
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National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                           CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Mark Raffeld, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert_Strausberg@nih.gov
          /organism="Lycopersicon esculentum"
/cultivar="VFNT cherry"
/note="organ: Leaf; Vector: pBluesc
/db_xref="taxon:4081"
/clone="CT093"
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/tissue_type="epidermis"
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/clone_lib="NCI_CGAP_Lym3"
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IMAGE:659237 5' similar to gb:M62419
protein (MOUSE);, mRNA sequence.
AA218212
                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393876.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -28m13 rev2 ET from Amersham.
Location/Qualifiers
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                                                                                                                                          Conservative
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/lab_host="SOLR (kanamycin resistant)"
                                               /tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
63 c 53 g 59 t
                                                                                                               /sex="unknown
                                                                                                                           /clone_lib="Soares mouse 3NME12 5"
                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
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21/ bp mRNA EST 03-JUN-1997 zv51h05:rl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757209 5', mRNA sequence.
AA444159
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Tel: (301) 496:1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 1585 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 195.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index.
Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:692655.
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/lab_host="DH10B"
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g677960
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1 (bases 1 to 217)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-Merck EST Project 1997

Unpublished (1997)

On Apr 14, 1993 this sequence version replaced gi:693545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 220)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read The vector to vector length is 218 seg primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                               HSC2TA072 nc
c-2ta07 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
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Fax: 314 286 1810
                                                                                                                                               F08804.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "/db_xref="GDB:5977822"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/note="Vector: pT7T3D-tac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:757209"
/clone_lib="Soares_testis_NHT"
/sex="male"
                                                                                                                                                                                                               220 bp mRNA EST 2: normalized infant brain cDNA Homo sapiens ', mRNA sequence.
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49 c 50
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 221)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                                                                                AA003770 221 bp mRNA
al59a06.sl Soares_NFL_T_GBC_S1 Homo
IMAGE:1461586 3', mRNA sequence.
AA883770
                                                                                              Tumor Gene Index
Unpublished (1997)
On Apr 14, 1993 th
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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95277534
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MAGE: molecular integration of the analysis of the human genome
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and its expression
                                                          Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 33169472800
Fax: 33160778698
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                                                            Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="total brain"
/dev_stage="3 months old"
33 c 42 g 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dept. Columbia University, USA. Bento Soares, P.N.A.S in press"
/db_xref="taxon:9606"
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/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="c-2ta07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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Pred. No. 2.23e+03;
0; Mismatches 0
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuqu Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                         Unpublished
On Sep 12, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence
AA881592
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                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                               MGI:667588
                                                                                                                               This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
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Similarity 100.0%;
                                                              primer: -28m13 rev2 ET from Amersham
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                    ished (1996)
12, 1996 this sequence version replaced
                                                                                                                                                                             mouseest@watson.wustl.edu
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="19; 806E08; 13; 13q22.3-13q31.3; 13p11.2-13q11"
/clone="IMAGE:1461586"
/clone_11b="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/lab_host="DH10B"
31 c 46 g 56 t
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clone IMAGE:1265036
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q597105
                                                                                                                                                                                                                                                                                              Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
                                                                                                                                                                                                                  Fax: 4169785650
Email: llewcc@utcc.utoronto.ca
Seq primer: GGTGGCGACGACTCCTGGAGCC
                                                                                                                                                                                                                                                                Banting Institute, 100 College St., Tel: 4169788758
                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                       Tsu1,S. and Lee,C.Y.
A catalogue of genes in the cardiovascular system as identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              95024171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T12418.1
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A275F Heart Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 100.0%;
Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     lew,C.C., Hwang,D.M., Fung,Y.W., Laurenssen,C., Cukerman,E.,
                                                                               57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
was primed with a Not I - oligo(dT) primer [5'
                                                                          /clone_lib="Heart"
/lab_host="E.coli Y1090"
55 c 65 g 4
                                                                                                                         /organism="Homo sapiens"
/note="Vector: Lambda gt:
/db_xref="taxon:9606"
/clone="A275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     provided by Dr. Bertrand Jordan. Library went through
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
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/lab_host="DH10B"
50 c 59 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:1265036"
/clone_lib="Soares 2NbMT"
                                                                                                                                                                                                 ocation/Qualifiers
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Pred. No.
0; Misma
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   Mismatches
                 DB 8; Le
2.23e+03;
                                                                                                                                                       gtl1; Site_1: EcoRI;
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                              Length 222;
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   0;
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RESULT

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Matches
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                                                                       92437550
AA603689.1
EST.
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np22h10.s1 NCI_CGAP_GC5 r
similar to SW:S10C_RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 69.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                            AA603689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                     Homo sapiens
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Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Organism="Homo sapiens"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
/note="Organ: pooled; Vector: Not I; Site_2: Eco RI;
a modified polylinker: Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were maxed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
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/lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/map="MMU16C3-C4 region; MMU16C3-C4 region"
/clone="IMAGE:1504720"
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Pred. No. 2.23e+03;
0; Mismatches 0
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Homo sapiens cDNA clone IMAGE:1117123
T P24480 CALGIZZARIN ;, mRNA sequence.
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                                                                                                                                                                                                                                                                             house mouse.
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 223)

1 (bases 1 to 223)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuquelsel, S., Kucabb, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 223)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397971.
                                                                 The WashU-HHMI Mouse EST Project Unpublished (1996)
On Jun 18, 1996 this sequence ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA646725 223 bp mRNA EST 28-OCT-1997 ve46h02.rl Soares mouse mammary gland NbMMG Mus musculus cDNA IMAGE:821235 5' similar to WP:F44E2.6 CE00184 TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 584 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 218.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATION ;, mRNA sequence.
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Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="germ cell tumor"
/lab_host="SOLR (kanamycin resistant)"
49 c 52 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1117123"
/clone_1ib="NCI_CGAP_GC5"
                                                                                                                                                                                                                                                                                                                                                                                                   GI:2573154
                                                                   this sequence version
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 224)

E 1 (bases 1 to 224)

E 2 (bases 1 to 224)

S Adams, M.D., Karlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzparald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Muyyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Collenan, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAJ58477 224 bp mRNA EST 21-APR-1998 EST79880 Placenta I Homo sapiens cDNA similar to similar to NADH-ubiquinone oxidoreductase, B22 subunit, mRNA sequence. AAJ68477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adaptors (Pharmacia), digested with Not I and cloned in
the Not I and Eco RI sites of the modified pT7T3 vector
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
50 c 60 g
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/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:821235"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares mouse mammary
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Pred. No. 2.23e+03;
0; Mismatches 0
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TITLE
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Best Local Similarity 100.0%;
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                                    RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clieyton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.G., Kelley, J.C., Liu, L.-I., Marmaros S.M., Werrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Phillips, C.A., Priggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarlk, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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EcoRI; Site_2: EcoRI"
/db_xref-"ATCC (inhost):173295"
/db_xref-"taxon:9606"
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53 c 58 q
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/tissue_type="placenta"
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Pred. No. 2.23e+03;
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Initial assessment of human gene diversity and expression patterns

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Local Similarity 100.0%;
hes 9; Conservative
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                                                                                                                                                          The Institute for Genomic Research 9712, Medical Center Drive, Rockvi
                                                                                                                                                                                                                                Unpublished (1998)
On Jan 17, 1998 this sequence version replaced gi:2044117
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Eutheria; Rodentia;
1 (bases 1 to 228)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST201407
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                                                                                                                                                                                                                                                                            Rat Genome Project: Generation of a Rat
                                                                                                                                                                                                                                                                                          Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Kerlavage,A.R. and Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                Rattus sp
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                                                                                                                                                                                                     Contact: Lee, NH
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Seq primer: M13 Reverse
                                                                                                il: nhlee@tigr.org
primer: M13-21.
                                                                                                                                (301)-838-3529
(301)-838-0208
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                                                                                                                                                                                                                                                                  Index
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7 Normalized
3' end, mRNA
                         /organism="Rattus sp."
/note="Organ: lung; Vector: pT7T3Pac;
Site_2: NotI"
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ECORI; Site_2: XhoI"
/db_xref-"ATCC (inhost):114131"
/db_xref-"taxon 9606"
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                                                                                     Location/Qualifiers
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41 c 75 g
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/cell_type="endothelial cell"
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Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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xref="ATCC (inhost):2015180"
|xref="taxon:10118"
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d. No. 2.23e+03;
Mismatches 0;
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                                          Site_1: EcoRI;
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180 TTCTGAGAA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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1 (bases 1 to 233)
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Seq primer: -40ml3
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mail: Robert_Strausberg@nih.gov
1ssue Procurement: W. Marston Linehan, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dec 30, 1996 this sequence version replaced gi:1529567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rt Length: 552 Std Error: 0.00 primer: -40ml3 fwd. ET from Amersham quality sequence stop: 97.
Location/Qualifiers
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     57
                                                                                                                                                                                                                          /Organism="Homo sapiens"
/Organism="Homo sapiens"
/note="Vector: pAMP10; Site_1: Not1; Site_2: ECORI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
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/dev_stage="45 years old"
/lab_host="DH10B"
51 c 56 g 69
                                                                                                                                                                                                     constructed by David Krizman."
                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:914094"
                                                                                     'sex="Male"
                                                                                                                clone_lib="NCI_CGAP_Pr1"
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AI000683
g3191237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 296 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2045877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 233)
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os64f02.sl NCI_CGAP_Br2
  AA552472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Similarity 100.0%;
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9; Conservative
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                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Br2"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
a 58 c 37 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                      {\tt NCI\_CGAP\_Br1.1.} Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. This library is the normalized version of
                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:1610139"
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2.23e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                  AA939036 235 bp mRNA EST 07-Ji op56g03.sl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone mage:1580884 3', mRNA sequence.
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On Sep 21, 1992 this sequence version replaced gi:276287
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Eutheria; Primates;
1 (bases 1 to 234)
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AA552472.1 GI:2322726
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                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                            Eutheria; Primates; 1 (bases 1 to 235)
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Similarity 100.0%;
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/db_xref="taxon:9606"
/clone="IMAGE:999793"
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/lab_host="DH10B"
59 c 53 g 69 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Prll"
/sex="male"
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                                                                                            Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1028 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 145.
Location/Qualifiers
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cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.

**DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

*www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA6Z1837 235 bp mRNA EST 21-OCT-1997 ng19e03.s1 NCI_CGAP_Thyl Homo sapiens cDNA clone IMAGE:1144348.
                                                                                                                                      Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                            Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:430445
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 235)
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AA621837
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/clone_1ib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
64 c 51 g 68 t
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32546 Lambda-PRL2
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MSU-DOE Plant Research Laboratory
Michigan State University
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h quality sequence stop: 227.
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/clone_11b="NCI_CGAP_Thy1"
/tissue_type="thyroid"
/lab_host="DH108"
a 38 c 57 g 48 t
                                /strain="var columbia"
/notee "Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/notee "Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/notee "Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/notee "Vector: lambda Zip-Lox; Site_1: Not;
/notee "Vector: lambda Zip-Lox; Not;
/notee "Vector: lambda Zip-Lox. The cDNA saliques. The vector is BRL's lambda Zip-Lox. The cDNA saliques.
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/organism="Homo sapiens"
/note="Vector: pAMP10; mRNA made from invasive thyroid
tumor, cDNA made by oligo-dT priming. Non-directionally
cloned. Size-selected on agarose gel, average insert size
600 bp. Reference: Krizman et al. (1996) Cancer Research
JARLY WET WESTER IS BRL'S LAMBDA Zip-Lox. The CDNA inserts were directionally cloned with Sal-Not arms using place drawther was "
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Matches 9; Conservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 159.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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AA627463.1 GI:2539558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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                                                                                                                                                                                                                 /note-"Organ: colon; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4). "
                                                                                           /clone="IMAGE:1147254"
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/lab_host="DH10B"
64 c 76 g 49 t
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/map="22; xp22.2; 18q12.3-q21.31"
/clone="215M17T7"
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47 c 60 g 6
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Score 9; DB 16.
Pred. No. 2.23e-
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25 ttctgagaa
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Bu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
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EST95699
AA382444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on Sep 1, 1995 this sequence version replaced
other_ESTs: EST95700 THC154392
                                                                                         h 100.0%;
Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bioinformatics
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Testis I Homo sapiens cDNA 3'
                                                                                                                                                                                                                                                                                                                       /note="Organ: testis; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):186776"
/db_xref="taxon:9606"
                                                                                                                                                                                                   /dev_stage="adult"
37 c 58 g
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                           ORGANISM
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                                                                                                                                                                                            AA253186 237 bp mRNA EST 06-AUG-1997 zr53f07.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667141
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                                                                                      EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        Homo sapiens
                                                                                                        AA253186.1
                                                                                                                                                   3', mRNA sequence.
AA253186
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 237)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/note="Organ: colon; Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from modified polylinker; 1st stranded cDNA was prepared from RER+ colon tumor, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco I sites of the modified pT/T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4). "
/db_xef="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1059461"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="colon tumor
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                                                                                                        GI:1882893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 bp
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IMAGE:1059461 3',
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AA339525
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washu-Merck EST project 1997
Unpublished (1997)
On Sep. 12, 1996 this sequence version replaced gi:1404755.
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanques,R.F., McDonald,L.A., Mguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 598 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 157.
Location/Qualifiers
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 239)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                     human.
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Similarity 100.0%;
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/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pTT3D-Pac
/note="Organ: mixed (see below); Vector: pTT3D-Pac
/Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G. E. clones 26023-265223,
340488-345479, and 484488-489479."
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/lab_host="DH10B"
/lab_host="DH10B"
46 c 47 g 64 t
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brain I Homo
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Pred. No. 2.23e+03;
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Local Similarity 100.0%;
nes 9; Conservative
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                   Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi/html)
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/note="Organ: brain: Vector: pBluescript SK-;
EcoRI; Site_2: XhoI"
/db_xref="haTCC (inhost):141139"
/db_xref="taxon:9606"
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/dev -
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61 c 72 g 45 t
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Fischer, C., nu.
Hudson, P.,
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1005)
                                     Genexpress-Genethon
Genethon Centre de recherche sur le Genome
1,rue de l'Internationale, BP60 91002 EVRY
Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242215 240 bp mRNA EST 08 HSCOCE011 normalized infant brain cDNA Homo sapiens c-0ce01, mRNA sequence.
                                                                                                                                                                                                                                                                             Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                                                                                       Eutheria; Primates; Catarrhini
1 (bases 1 to 240)
Auffray, C., Behar, G., Bois, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Email: genexpress@genethon.fr
Single read.
                                                                                                                                          Contact: Genethon
                                                                                                                                                                                On Sep 21, 1992 this
                                                                                                                                                                                                    95277534
                                                                                                                                                                                                                                                          IMAGE: molecular integration of the
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Similarity 100.0%;
9; Conservative
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Fax: 3018699423
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/db_xref="taxon:9606"
/clone_lib="Supt cells"
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49 c 5
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, Rockville,
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2.23e+03;
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                                                                                                                                                                                                                   318 (2), 263-272 (1995)
                                                                                                                                                                                                                                                          analysis of the human genome
                                                                                                                                                                             replaced gi:279052
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E 1 (bases 1 to 241)

E Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., HinkleJT, P.S., Kelley, J.M., Kilmek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of CDNA Sequence
                                                                    Other_ESTs: THC23264
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 2
Tel: 3018699056
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T29421.1
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Seq primer: (-21)M13_universal.
Location/Qualifiers
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Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
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/db_xref="taxon:9606"
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28mi3 rev2 ET from Amersham

High quality sequence stop: 238.

Location/Qualifiers
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WashU-Merck EST Project 1997
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Hillian T ...
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Fax: 314 286 1810
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                                                                                                                                                                                  /organism="Homo sapiens"
/notce="Organ: placenta"
/db_xref="ATCC (inhost):106211"
/db_xref="taxon:9606"
/clone_lib="Human Placenta"
a 32 c 76 g 90 t
/clone="IMAGE:797037"
/clone_11b="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
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/map="797C03; 14; x"
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F12521.1
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1 (bases 1 to 242)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Rabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex,
Tel: 33169472800
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HSC3BAll1 normalized
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                  /organism="Homo sapiens"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5′ -> 3′ into the HindIII -> NotI sites of the
cloned 5′ -> 3′ into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
/db_xref="taxon:9606"
                                                                                                                 /tissue_type="total brain"
/dev_stage="3 months old"
49 c 64 g 66 t
                                                                                                                                                            /sex="Female"
                                                                                                                                                                            /clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                        /map="947H01; 11; 11p12-11p14.1"
/clone="c-3ball"
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                                                         Mus musculus
Eukaryota; Metazoa; (
Eutheria; Rodentia; S
1 (bases 1 to 243)
1 (bases 1 to 243)
1 (bases 1 to 243)
                                                                                                                                                                                                                                                                    AA408476 243 bp mRNA EST 26-7 EST02957 Mouse 7.5 dpc embryo ectoplacental cone cDna musculus cDNA clone C0028F01 3' similar to R.rattus mi ribosomal protein L11, score - 968, mRNA sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 243)
Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and
Rapid CDNA sequencing (expressed sequence tags) from a
directionally cloned human infant brain cDNA library
Acture Genet. 4, 373-380 (1993)
Nakashima,H.
Systematic analyses
                                                                                                                                                                                                                                                   ribosomal protein
AA408476
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Fax: 3018699423
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                                          Pryor, E., Paris, J.,
                                                                                                                                                                  house mouse.
                                                                                                                                                                                                          AA408476.1 GI:2067872
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/note="Organ: spleen; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):143690"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Fetal spleen"
/dev_stage="fetus"
40 c 54 g 47
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    of mouse genes
                                          Wells-Smith, J.,
                                                                                                      Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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                                          Horton, J.H., Wang, X, Cui, Y., ls-Smith, J., Fujiwara, H., Yot
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                                          Yotsumoto, S. and
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                                Contact: Marra M/Mouse EST Project
'Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
                                                                                                                                                                                                                                         Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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1 (basss 1 to 243)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S.; Kucaba,T., Lacy,M., Le,M., Martin,J., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
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vt81d04.rl Barstead m
clone IMAGE:1177543 5
AA759834
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On Sep 12, 1996 this sequence version replaced gi:1395293.
                                                                                                                                                        The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 9, 1998 this sequence vers
                                                                                                                                                                                                                                  Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                  EST
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R.rattus mRNA for ribosomal protein Lil, score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           g2807628
                                                                                                                                                                                                                                                                                                                                                                                                 house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: embryo; Vector: pSPORTI (Life Technologies); Site_1: Sali, Site_2: Noti; Total RNAs were extracted from ectoplacental cone of 7.5-dpc embryos. The double-stranded cDNA was synthesized from total RNAs with an Oligo(dT) primer. The library was constructed by Minoru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="ATCC (inhost):1364379"
/db_xref="taxon:10090"
/clone="C0028F01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="ectoplacental cone"
/dev_stage="embryonic day 7.5 post
/lab_host="DH10B"
/1ab_63 c 56 g 75 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:2807628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST mouse irradiated colon MPLRB7 5', mRNA sequence.
                                                                                                                                                        sequence version
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Pred. No. 2.23e+03;
0; Mismatches 0;
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Total RNAs were extracted from
pc embryos. The
                                                                                                                                                        replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 243;
                                                           Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 others
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                                                                                                                                                      g1:936878
                                                           MO 63108
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                                                                              FEATURES
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source

/organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand

CDNA

Seq primer: -40ml3 fwd.

ET from

Amersham

Cocation/Qualifiers

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AUTHORS
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 ttctcagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
           CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R.
                                                                                                                                                                                                                                              Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
AA809659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA809659 245 bp mRNA
nk96d07.s1 NCI_CGAP_CO3 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                               M.D., Ph.D.
                                                                                                                                                                                                                            On Jan 19, 1998
                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                         ĀA809659.1 GI:2879065
                                                                                                                                                                                                                                                                                                                          (bases 1 to 245)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Barstead mouse irradiated
/dev_stage="8 weeks"
/lab_host="DH10B"
53 c 43 g 54 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                                                                                                                            this sequence version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1st strand cDNA was primed
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                                   Sequencing Center information can be
                                                                                                                                                                                                                                                                                      Project (CGAP),
                                                                                                                                   Emmert-Buck,
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Matches 9; Conservative
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25 ttctgagaa
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Sasaki,T., Miyao,A. and Yan
Rice cDNA from callus 1995
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa Oryza sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Enbryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Oryza.
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D47177.1 GI:700886
EST.
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RICS13347A Rice green shoot Oryza sativa cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                Email: tsasaki@abr.affrc.go.jp
Insert Length: 373 Std Error: 0.00
High quality sequence stop: 327.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                               National Institute of Agrobiological Resources Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                               Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
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/clone_lib="NCI_CGAP_Co3"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
a 72 c 60 g 49 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization.
                                                                                                                                                        /strain="Nipponbare"
/note="Green shoot (8 days old)"
/db_xref="ftaxon:4530"
/clone_lib="Rice green shoot"
/clone_lib="74 g 64 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="13"
                                                                                                                                                                                                                                                    organism-"Oryza sativa"
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                                                                   Score 9;
Pred. No.
0; Misma
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Pred. No. 2.23e+03;
0; Mismatches C
                                                                       Mismatches
                                                                                      DB 19; I
2.23e+03;
                                                                                                     Length 246;
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Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Claytou, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., HinkleJIr, P.S.,
Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
                                                                                                                       vs52cl2.rl Stratagene mouse Tcell 937311
IMAGE:1149910 5', mRNA sequence.
AA822615
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EST23709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056
  house mouse. Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 3018699423
Email: tdbinfoetdb.tigr.org
Emore clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other_ESTs: THC9931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)
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                                                                            AA822615.1 GI:2892483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Homo sapiens"
/db_xref="ATCC (inhost):100804"
/db_xref="taxon:9606"
/clone_lib="Human Bone"
/tlssue_type="bone"
38 c 40 g 96 t
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Pred. No. 2.23e+03
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Mus musculus cDNA clone
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 247)
1 (bases 1 to 247)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                    vn12h05.rl Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1021017 5', mRNA sequence.
AA646505
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1 (bases 1 to 246)
Marri, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                             Unpublished
                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                     AA646505.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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h quality sequence stop: 151.
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314 286 1810
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/note="Organ: blood; Vector: pBluescript SR-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Stratagene mouse Tcell 937:
/tlssue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
68 c 50 g 56 t
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this sequence version replaced
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Pred. No. 2.23e+03;
0; Mismatches 0
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Fax: 314 286 1810
CDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lini.gov/bbrp/image/image.html
                                                                                                                         Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393648
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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AA565709
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nk47h12.sl NCI_CGAP_GC2
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Similarity 100.0%;
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National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                           numan.
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                                                                                                         cDNA Library Preparation: Stratagene, Inc.,
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Location/Qualifiers
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/lab_host="SOLR (kanamycin resistant)"
67 c 75 g 47 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="pooled"
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/strain="NIH/Swiss"
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| 25 ttctgagaa 33
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Balt.C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehn, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Weil, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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AA344114
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
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Similarity 100.0%;
9; Conservative
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                     Contact: Kerlavage, AR
                                                                                                                                                                                                                On Apr 14, 1993 this sequence version replaced gi:716386.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:501924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA872080 250 bp mRNA EST 17-MAR-1998 oil2all.sl NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1476284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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                                                                                    /organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
AI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
/db_xref="taxon:9606"
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Site_1: EcoRI: Site_2: XhoI"
/db_xref="ATCC (inhost):145639"
/db_xref="taxon:9606"
                                          /map="22"
/clone="IMAGE:1476284"
/clone_lib="NCI_CGAP_GC4"
/tissue_type="pooled_germ_cell_tumors"
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76 c 43 g 55 t
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/clone_lib="Gall bladder I"
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High quality sequence stop: 203.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy
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 AA343598
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                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                    /note="Vector: pamp10; mRNA made from alveolar rhabdomyosarcoma, cDNA made by oligo-dr priming. Non-directionally cloned Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
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48 c 57
                                                                                                                                                                                                                     /clone_lib-"NCI_CGAP_Alv1"
/tissue_type-"alveolar rhabdomyosarcoma"
/lab_host="DH10B"
68 c 64 g 60 t
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/clone="IMAGE:1206654"
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
AL Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                             87
                                          o182a08.s1 Soares_NFL_T_GBC_S1 Homo IMAGE:1504790 3', mRNA sequence. AA905871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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AA343598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Apr 14, 1993 this sequence version replaced g1:693051 Other_ESTs: THC137512
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/note="Organ: gall bladder; Vector:
Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):145109"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Gall bladder I"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
GI:3040994
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Pred. No. 2.23e+03;
0; Mismatches 0
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Best Local Similarity 100.0%;
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                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 9, 1998 this sequence version replaced gi:934519.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.lovo) for further information.
Insert Length: 726 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 66.
                        Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 254)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: Robert_Strausberg@nih.gov
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//clone="INAGE:1504790"
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/lab_host="DH10B"
52 c 49 g 85 t
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Pred. No. 2.23e+03;
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High quality
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                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih ~~"
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Email: Robert_Strausberg@nih.gov
This clone is available royally free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 119.
                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
On Feb 10, 1998 this sequence version replaced gi:2339903.
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1 (bases 1 to 254)
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Similarity 100.0%;
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/tlssue_type="germinal center B cell"
/tlsb_host="DH10B"
/lab_host="DH10B"
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Pred. No.
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Best Local
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Seq primer: -40m13 fwd. ET from Amers
Location/Qualifiers
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AA527319
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                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                             Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Unpublished (1997)
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Eutheria: Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 255)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1623003"
/clone_1lb="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
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49 c 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40ml3 fwd. ET from
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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grade"
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/lab_host="DH10B"
39 c 40 q
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/clone="IMAGE:936849"
/clone_11b="NCI_CGAP_Co3"
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34 c 41
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/clone_lib="NCI_CGAP_Pr4.1"
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                                  TTCTGAGAA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 152.
Location/Qualifiers
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. washU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AA429636
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Similarity 100.0%;
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/organism-"Homo sapians"
/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
                                                                                                                                                                /lab_host="DH108"
44 c 39 (
                                                                                                                                                                                                                                       constructed by Bento Soares and M.
/db_xref="taxon:9606"
/clone="IMAGE:781977"
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AA496492
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AA991905
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1407356
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 261)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,
                                                                                                           EST
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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1 (bases 1 to 259)
                                                                    Homo sapiens
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National Cancer Institute, Cancer Genome Anatomy
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone="IMAGE:1611312"
/Clone_11b="NCI_CGAP_GC2"
/tissue_type="germ_cell_tumor"
/lab_host="SOLR_(kanamycin_resistant)"
58 c 62 g 66 t
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id. No. 2.23e+03;
Mismatches 0;
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Unpublished (1997)
On Sep 21 1000
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EST65872
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                                                                                                         On Sep 12, 1996 this sequence version replaced gi:1288030 Other_ESTs: THC181248
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 261)

Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C. Rapid CDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library discurre Genet. 4, 373-380 (1993)
                                                    The Institute for Genomic 9712 Medical Center Drive,
                                                                               Bioinformatics
                                                                                            Contact: Kerlavage,
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
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Fax: 314 286 1810
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            arkerlav@tigr.org
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Jurkat T-cells
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/db_xref-"taxon:9606"
/clone-"IMAGE:755701"
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/lab_host="DH10B (ampicillin resistant)"
71 c 52 g 68 t
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Initial assessment of human gene diversity and expression patterns based upon 8 million nucleotides of cDNA sequence on Apr 14, 1993 this sequence version replaced gi:693436.

On Apr 14, 193 this sequence version replaced gi:693436.
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Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seg primer: M13 Reverse.
                                                                                       Email: arkerlayetigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                            9712 Medical Center Drive, Tel: 3018699056
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                                                                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                    Contact: Kerlavage, AR
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/clone_lib="Jurkat T-cells I"
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∕organism="Homo sapiens"
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1 (bases 1 to 262)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S. Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washb-NCI human EST Project

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA721968 262 bp mRNA ES
zh17b04.s1 Soares_pineal_gland_N3HPG Homo
IMAGE:412303 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                3'], double-stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
/db_xref="GDB:1303997"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/organism="Homo sapiens"
/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
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ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):187991"
/db_xref="taxon:9606"
                                                                                                                                                /cione_lib-"Soares_pineal_gland_N3HPG"
/lab_host="DH10B (ampicillin resistant)"
62 c 64 g 69 t
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58 c 55 g
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/sex="male"
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    100.0%;
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No. 2.23e+03;
DB 17; Length 262; 2.23e+03;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                    ttctgagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mmarra@watson.wustl.edu

PCR_E: TGTAAAACGACGCCAGTGACCAAGGTTCCAGCCTGG

PCR_B: CAGGAAACAGTATGACCCTTATGAGTATTTCTTCCAGGGTA

Source: Washington University Genome Sequencing Center

PCR amplified DNA is available from Washington University Genome

Sequencing Center. Aliquots of the library may be requested from Insert Length: 494 Std Error: 0.00

Seq primer: Commercially available M13 reverse dye primer

High conditions are aliquots washington the primer of the conditions of the library may be requested from Insert Length: 494 Std Error: 0.00
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University Genome Sequencing Center Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University Caenorhabditis briggsae EST project Unpublished (1995)
Other_ESTs: pk08c03.s1
Contact: Marra MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier,L., Chiapelli,B., Chissoe,S., Clark,N., Couch,J.,
Dubuque,T., Hawkins,M., Holman,M., Hultman,M., Kucaba,T.,
Kuwabara,P., Le,M., Mardis,B., Marra,M., Parsons,J., Rikin,L.,
Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Wohldmann,P. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi (bases 1 to 263)
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cDNA, mRNA
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                      /note="Vector: Lambda gt10; Site_1: EcoRI; Site_2: EcoRI; Stage:mixed, Sex:hermaphrodite. Library construction: First strand oligo(dT) primed. Second strand was as per Gubler/Hoffman. Ligated to EcoRI adaptors. Library is non-directional. Library is non-normalized. Library constructed by P.E. Kuwabara. Additional details on construction of the library are described in P.E. Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor sequence: GAATTC CGTTGCTGCG"
                                                                                                                                                                                                                                                                               /clone_lib="Kuwabara Mixed Stage C. briggsae"
56 c 54 g 69 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="G16 Gujarat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Caenorhabditis briggsae"
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2.23e+03;
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  12-MAR-1997
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Local Similarity 100.0%;
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                       ttctgagaa 33
                                                                                                                                                                                                                      AA525063 263 bp mRNA EST 05-AUG-1997 nh32g03.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:954100 similar to 9b:S41458 ROD CCMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 263)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:400455
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
On Sep 12, 1996 th
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mv10b04.rl GuayWoodford Beier clone IMAGE:654607 5' similar
                                                                                                                                              AA525063.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -28ml3 revl ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:654607"
/clone_lib="GuayWoodford Beler mouse kidney day
/tissue_type="kidney"
/dev_stage="newborn (day 0)"
/lab_host="SOLR (kanamycin resistant)"
67 c 76 g 56 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lisa Guay-Woodford."
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2.23e+03;
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                                                                                                                                                                                                                                                                                                                                                                              264 bp mRNA
CELK032E9R Yuji Kohara unpublished
clone yk32e9 3', mRNA sequence.
D33548
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:785493
Unpublished (1994)
On Sep 21, 1992 this sequence version replaced g1:279326
                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                           Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 264)
                                                                                                                                                                                                                                                                                                                          D33548.1 GI:524467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 263)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 88.
Location/Qualifiers
                                                                                       Tabara, H
                                                                                                               Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T.,
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Similarity 100.0%;
9; Conservative
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                                                         an expression map of the C.elegans
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/lab_host="DH10B"
50 c 53 g 78
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0; Mismatches
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cDNA Caenorhabditis elegan:
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LOCUS
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HSC1HB102 normalized
c-1hb10 3', mRNA serve
Z39705
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239705.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria: Primates: Catarrhin; Hominidae; Homo.

1 (bases 1 to 264)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,

Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,

Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,

Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                         Single read. 28 T removed at sequence 5'end Genexpress_library_idt: C; Genexpress_sequence_idt: alc-lhb10 Seq primer: (-21)M13_universal.
                                                                                                                                                                                                                                                                   Email: genexpress@genethon.fr
Single read. 28 T removed at
                                                                                                                                                                                                                                                                                                     Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de 1'Internationale, BP60 91002 EVRY Cedex,
Tel: 33169472800
Fax: 33160778698
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National Institute of Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 100.0%;
Similarity 100.0%;
9; Conservative
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R. Acad. Sci. I
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                               /Organism="Homo sapiens"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
/db_xref="taxon:9606"
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tissue_type=whole_animal"
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/clone="yk32e9"
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/strain="CB1489 him-8(e1489)"
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2 : 5
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IS CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                         vector to vector length is
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 514 200 2000
Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
On Sep 21, 1992 this sequence version
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9; Conservative
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(bases 1 to 264)
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                                                  /organism="Mus musculus"
/strain="C5TBL/6J"
/note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
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/dev_stage="3 months old"
45 c 44 g 70
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/sex="Female"
                 /db_xref="taxon:10090"
/clone="IMAGE:718460"
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'clone_lib="Soares mouse lymph node NbMLN"
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 ttctcagaa 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
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1 (bases 1 to 264)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: washington University Genome Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
Tissue Procurement: Lee Helman, Ph.D., Michael Emmert-Buck, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
On Apr 14, 1993 this sequence version replaced g1:837673
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Similarity 100.0%;
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/note="Vector: pCMV-SPORT2; Site_1: Sal; Site_2:
Cloned unidirectionally. Primer: Oligo dT."
/db_xref="GDB:6029006"
                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:803134"
/clone_11b="NCI_CGAP_AR1"
/tissue_type="bulk alveolar tumor"
/lab_host="DH108"
34 c 49 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
/tissue_type="lymph node"
/dev_stage="4 weeks"
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61 c 50 g
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 265)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Insert Length: 846 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 195.
Location/Qualifiers
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Email: Robert
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                                                                        AA603628 266 bp
np19g01.sl NCI_CGAP_Br3
mRNA sequence.
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On Sep 12, 1996 this sequence version replaced gi:1402085
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Similarity 100.0%;
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: polyllar cells enriched for was prepared from human tonsiliar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI), Dr. David Allman (NCI)
                                                                                                                                                                                                                                                                                                                                                          /tissue_type-"germinal
/lab_host-"DH10B"
84 c 66 g
                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                 Score 9; DB 10; L
Pred. No. 2.23e+03;
0; Mismatches 0
                                                                                            mRNA EST
Homo sapiens cDNA clone
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Local Similarity 100.0%;
ses 9; Conservative
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Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                         Unpublished (1997)
On Jan 24, 1995 th
                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 266)
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AA904030
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oe74e11.s1 NCI_CGAP_Lu5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: L. J
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                 Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/note="Organ: breast; Vector: Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Ductal breast tumor. 5' adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTT 3' Average insert size: 0.9 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="breast tumor"
/lab_host="SOLR (kanamycin resistant)"
48 c 38 g 93 t 1 oth
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/clone_11b="NCI_CGAP_B
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                                                         replaced gi:634370
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MBL2SUBC9T3 Brugia malayi second stage larvae JHU96SL-BmL2
malay1 cDNA clone L2SUBC9 5', mRNA sequence.
AA241715
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
Tel: +44 131 650 6760

Fax: +44 131 670 5450

Email: mark.blaxtered.ac.uk

The ABI trace of this sequence can be viewed at

http://www.sanger.ac.uk/Drugia/L2S/MBL2SJ8C9T3.html This is the
full sequence of the cDNA clone. The polyA tail has been clipped
and is excluded from this sequence
                                                                                                                                                                   Contact: Blaxter ML Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, 3JT, UK.
                                                                                                                                                                                                                                                                                                                Genes expressed in adult female Brugia malayi
Unpublished (1996)
On Jun 18, 1996 this sequence version replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brugia malayi
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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Seq primer: -40m13
High quality sequer
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                                                                                                                                                                                                                                                                                                                                                                                                                  Blaxter, M.L., Waterfall, M., Daub, J., Lizotte, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 266)
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Similarity 100.0%;
9; Conservative
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Pred. No. 2.23e+03;
0; Mismatches 0;
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Best Local Similarity 100.0%;
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                                                                                        MGI:399893
Seq primer
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1 (bases 1 to 270)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA197883 270 bp mRNA EST 12-MAR-1997 mv04b11.rl GuayWoodford Beier mouse kidney day 0 Mus musculus cDNA clone IMAGE:654045 5' similar to TR:G406113 G406113 PROTEIN KINASE
                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashUrHHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. ;, mRNA sequence.
AA197883
                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
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                                                          primer: -28m13 rev1 ET from Amersham
h quality sequence stop: 229.
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/organism="TRS Labs"
/strain="TRS Labs"
/note="Vector: lambdaZapII; Site_1: Eco R I (5' end);
/note="Vector: lambdaZapII; Site_1: Eco R I (1' end);
/note="Vector: lambdaZapII; Site_1: lambdaZapII; lambda
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Location/Qualifiers
1. 270
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JHU96SL-BmL2"
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/lab_host="E. coli XL1-Blue MRF-"
37 c 51 g 98 t 5 others
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1. .266
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/clone="L2SJ8C9"
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Pred. No. 2.23e+03;
0; Mismatches (
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                             source
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Allen, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1325182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA276995 270 bp mRNA EST 01-APR-1997 va25h12.rl GuayWoodford Beier mouse kidney day 7 Mus musculus cDNA clone IMAGE:732455 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.linl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA276995.1 GI:1919631
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Location/Qualifiers
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                                                    /note="Organ: kidney; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: xhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP xR Vector; -5; adaptor sequence: 5; GAATTCGGCACGAG 3 -3; adaptor sequence: 5; CTCGAGTTTTTTTTTTTTTTTTT 3; Library provided
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/db_xref="taxon:10090"
/clone="IMAGE:654045"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/clone_lib="GuayWoodford Beier mouse kidney day 7"
/tissue_type="kidney"
                                                                                                                                                                                                                                                                                                                                            'organism="Mus musculus"
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_host="SOLR (kanamycin resistant)"
62 c 74 g 71 t
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Pred. No. 2.23e+03;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                  TTCTGAGAA 13
ttctgagaa 33
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Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown library type
Insert Length: 1426 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AA642354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Similarity 100.0%;
9; Conservative
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                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:1185062"
/clone_1ib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
71 c 61 g 74 t
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58 c 70
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Pred.
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Pred. No. 2.23e+03;
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No. 2.23e+03;
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                                                                                                                                          AA182421 271 bp . mRNA EST 10-MAR-1998 zp56f02.rl Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:613467 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   v172c09.r1 Stratagene mouse testis (#937308) Mus musculus clone IMAGE:917776 5', mRNA sequence.
AA497742
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On Dec 18, 1996 this sequence version
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Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa;
Eutheria; Rodentia;
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                         g1766304
                                                                                                                           AA182421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 252.
Location/Qualifiers
                                                                                        AA182421.1 GI:1766304
                                                                                                                                                                                                                                                                                                                      h 100.0%;
Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
84 c 63 g 53 t
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Pred. No. 2.23e+03;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                         Length 271;
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KEYWORDS
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TITLE
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JOURNAL
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Best Local Similarity 100.0%;
                                                                                                                                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 TTCTCAGAA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttctcagaa 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 3799 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 127.
                          Tel: (301) 496-1550
Email: Robert_Straus
Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 271)
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Hillar,L., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Unpublished (1997)
                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                              Unpublished (1997)
On Sep 21, 1992 this sequence version replaced g1:276412
                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 272)
                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                       AA640402 272 bp mRNA EST 27-OCT-1997 nt99e05.sl NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1206656,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
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                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                          AA640402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
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                                                                                                                                                    Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Stratagene NT2 neuronal precursor /tissue_type="neuroepithelial cells" /dey_stage="Ntera-2 neuroepithelial cells" /lab_host="SOLR (kanamycin resistant)" /lab_host="SOLR (kanamycin resistant)" / 49 c 81 g 54 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:613467"
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                                                                                                                                                                                                                                                                                                          GI:2565652
                            Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
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Pred.
0; M
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David B.
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2.23e+03;
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Krizman,
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Ph.D
                                                                                                                                                                  Project (CGAP),
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SOURCE
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LOCUS
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Watch 100.0%; Local Similarity 100.0%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 273)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque,;
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2286559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ua60h12.s1 (
similar to (
AA990483
g3175847
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High quality sequence stop: 143.
Location/Qualifiers
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                         Possible reversed clone: similarity on wrong Possible reversed clone: polyT not found Seq primer: -40ml3 fwd. ET from Amersham. Location/Qualifiers
                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                  MGI:699967
                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
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/note="Vector: pAMP10; mRNA made from alveolar
/nbtbe="Vector: pAMP10; mRNA made from alveolar
rhabdomyosarcoma, cDNA made by oligo-dT priming.
rhabdomyosarcoma, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Reference: Krizman et al.
(1996) Cancer Research 56:5380-5383."
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/clone="IMAGE:1206556"
/clone_11b="NCI_CGAP_Alv1"
/tlssue_type="alveolar rhabdomyosarcoma"
/tab_host="DH10B"
/lab_host="DH10B"
/9 c 67 g 65 t
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT7T3D-Pa
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SW:G10_XENLA
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Pred. No. 2.23e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus cDNA clone IMAGE:1361927 P12805 G10 PROTEIN. ;, mRNA sequence.
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pT7T3D-Pac (Pharmacia) with a modified

1 others

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236 TTCTCAGAA 244
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                                                                                                                                                                                                                                                                                                                                                On Nov 29, 1993 this Other_ESTs: TC45098
                                                                                                                                                                                                                                                                                                                                                                                                                               Fuldner,R.A., Marmaras,S., Glodek,A., Gocayne,J.D., Adams,M.D., Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 274)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus sp.
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g2671547
AA684949.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA684949 274 bp mRNA EST 03-APR-1998 EST105836 Rat PC-12 cells, untreated Rattus sp. cDNA clone RPCAT58 5' end similar to Elongation factor 1 gamma, mRNA sequence.

AA684949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 100.0%;
Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 factor treatment
                                                                                                                                                                                                                il: nhlee@tigr.org
primer: M13 Reverse.
                                                                                                                                                                                                                                                 (301)-838-3529
(301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                  Natl. Acad. Sci. U.S.A.
                                           /organism="Rattus sp."
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
xhoI; poly(A)+ RNA was purified from untreated PC12 cells
cultured for 9 days. cDNA was constructed using an
oligo-dT primer and directionally cloned using the Lambda
ZAP II Vector Kit by Stratagene"
/db_xref="ATCC (inhost):2000826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
77 c 73 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares 2NbMT"
/sex="male"
/clone_lib="Rat PC-12
               /clone="RPCAT58"
                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1361927"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xref="taxon:10090"
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Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                 sequence version replaced gi:502312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Leus
2.23e+03;
-hes 0;
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cells, untreated"
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                               ttctgagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Ailen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washr-Merck EST Project 1997
Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:692564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 223.
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Eukaryota; M
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                                                                                             h 100.0%;
Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                              /sex="Female"
                                                                                                                                                                                                                                                                  /clone="IMAGE:754931"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Matches 9; Conservative
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AA282274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Emoil: arkerlav@tigr.org
Emoil: arkerlav@tigr.org
Emoil: arkerlav@tigr.org
Emoil: arguence and expression
Information related to this EST, please check the TIGR Human Gene
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Information related to this EST, please check the TIGR Human Gene
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EST.
                   Tumor Gene Index
Unpublished (1997)
                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 276)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Apr 14, 1993 this sequence version replaced gi:635723. Other_ESTs: THC177532
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29, 1993 this sequence version replaced gi:430552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Adipose tissue, white I"
/tissue_type="adipose tissue, white"
/dev_stage="adult"
/dev_stage="adult"
74 c 55 g 52 t 6 of
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/db_xref="taxon:9606"
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/note="Vector: pBluescript SK-;
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1 (bases 1 to 277)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Rabaktchis,C. and Tessier,A.

Sebastiani-Rabaktchis,C. and Tessier,A.
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F10065.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 277
Seq primer: -28ml3 rev2 ET from Amersham.
                              Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de 1'Internationale, BP60 91002 EVRY Cedex,
Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSC3AB042 normalized infant brain cDNA Homo c-3ab04 3', mRNA sequence.
                                                                                                                Contact: Genethon
                                                                                                                                               On Sep 21, 1992 this sequence version replaced gi:278956
                                                                                                                                                                  95277534
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read. removed at sequence 5'end
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/lab_host="DH10B"
63 c 75 g 61 t
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/clone_lib="NCI_CGAP_GCB1"
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On Jan 19, 1998 this sequence version replaced g1:2152365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                             Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 277.
                                                                                                                                                                                                                                                                                                                                      Tissue Procurement:
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                                                                                                                                                                                                                                                                                                                    Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                    cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                   (301) 496-1550
L: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; 'isolate=muscular atrophy patient: tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5', 3' into the HindIII-> NotI sites of the lafmid BA vector. Clone library from B. Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"

/db_xref="taxon:9606"
             /dev_stage="3 months old"
48 c 52 g 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
/tissue_type="total brain"
double-stranded cDNA was ligated to Eco
                                                                                            organ:
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                                                                                                                                                                                                                                                                                                                                      Christopher Moskaluk, M.D., Ph.D.,
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d. No. 2.23e+
Mismatches
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2.23e+03;
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Similar to SW:YA94_SCHPO Q09783 HYPOTHETICAL 11.4 KD PROTEIN
C13G6.04 IN CHROMOSOMF 1 TO THE TOTAL TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., F
Ph.D., Gerald Marti, M.D.
cDNA_Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2152693
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1 (bases 1 to 279)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 486
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Similarity 100.0%;
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Location/Qualifiers
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/Organism="Homo sapiens"
//organism="Homo sorting (CD20 RI; lst strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-),
//organism="Homo human tonsillar cells enriched for yell-a, representation of the coll of the coll of the synthesis was primed with a Not I - oligo(dT) primer
//organism="Homo sapiens"
//organisms
//organis
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/clone_1ib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors
/lab_host="DH10B"
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2.23e+03;
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Best Local Similarity 100.0%;
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DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allmi
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 279)
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Seg primer: -40m13 fwd.
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                                                                                                                                                                                                                                                                                                                                                                 primer: -40m13 fwd. ET from Amersham
quality sequence stop: 239.
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                            3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="IMACE:1298823"
                                                                                                                                                           /tissue_type="germinal center /lab_host="DH10B" 73 c 57 g 79 t
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/clone_lib="NCI_CGAP_GCB1"
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                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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2.23e+03;
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32 TTCTCAGAA 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 457 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 272. Location/Qualifiers
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CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Unpublished (1997)
On Jan 17, 1998 th
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co38a11.s1 NCI_CGAP_Lu5
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1 (bases 1 to 280)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from modified polylinker; lst strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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68 c 53
                                                                                                                                   /tissue_type="carcinoid"
/lab_host="DH10B"
68 c 70 g 6
                                                                                                                                                                                                /clone_lib-"NCI_CGAP_Lu5"
                                                                                                                                                                                                                   clone="IMAGE:1568444"
                                                                                                                                                                                                                                                          'db_xref="taxon:9606"
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Homo sapiens cDNA clone IMAGE:1568444
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                                                                                                                                                                                                                                                          Y Match 100.0%;
Local Similarity 100.0%;
los 9; Conservative
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                 vl46a10.sl Stratagene mouse skin
IMAGE:975258 3', mRNA sequence.
AA589358
g2402738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LINL; contact the IMAGE Consortium (info!mage.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 266.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 280)
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Fax: 314 286 1810
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/db_xref="QDB:5930920"
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/note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDl was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not: I - oligo(dT)
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67 c 66 g
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/clone="IMAGE:743632"
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GI:2402738
                                                                                                 280 bp
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Pred. No. 2.23e+03;
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                              AUTHORS
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced ai. 1404840
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Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                   AA302617 282 bp mRNA EST 18-APR-1997 EST15792 Aorta endothelial cells Homo sapiens cDNA 5' end sim: to similar to EBER-associated protein, mRNA sequence.

AA302617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
house mouse.
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
                                                                                                                                                                                           AA302617.1 GI:1954948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 189.
                                                             Eutheria; Primates;
1 (bases 1 to 282)
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                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: polyT not found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
62 c 56 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
                                                                                   Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
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Le,M., Martin,J., Morris,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 280;
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence of cDNA sequence of the property of this sequence version replaced gi:1366592.
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Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
                                                                                                                                     Eukaryota; Metazoa;
Eutheria; Rodentia;
1 (bases 1 to 283)
                                                                                                                                                                                                                                                                                                                                                           AI012299 283 bp mRNA EST206750 Normalized rat placenta, Bento clone RPLAV23 3' end, mRNA sequence.
  Unpublished (1998)
On Jan 19, 1998 this
                                                                     Rat Genome Project:
                                                                                                                                                                                                                     Rattus sp.
                                                                                                                                                                                                                                         Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                        AI012299.1
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Similarity 100.0%;
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/note="Organ: aorta; Vector: pBluescript SK-;
EcoRI; Site_2: XhoI"
/db_xref="harCC (inhost):114794"
/db_xref="taxon:9606"
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48 c 66 g
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/cell_type="endothelial cell"
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                                                                          Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                   Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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sequence version replaced g1:2285611
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2.23e+03;
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Soares Rattus sp. cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. B.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Sep 12, 1996 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Butheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 283)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
AA652376
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Seq primer: M13-21.
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Fax: (301)-838-0208
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Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sep 12, 1996 this sequence version replaced gi:1397808
/note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; ist strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT773 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
/db_xref="taxon:9606"
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/note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: Not!"
/db_xref="taxon:10118"
/clone="RPLAV23"
                                                                                                                                                                                  /organism="Homo sapiens"
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83 c 81 g
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Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.23e+03
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59 t
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                                                                                       Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Hum
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 12, 1996 this sequence version replaced gi:1326766 Other_ESTs: THC177442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 283)
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EST112537 Adrenal gland tumor Homo sapiens cDNA 5' end, mRNA
                                                                                                                                                                                                     Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                             3018699056
                     /note="Organ: adrenal gland; Vector: pBluescript SK-; Site_1: ECORI; Site_2: XhoI" /db_xref="ATCC (inhost):120252" /db_xref="taxon:9606"; 120252"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
47 c 57 g
                                                                                                                              /organism="Homo sapiens"
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/clone="IMAGE:1187297"
'clone_lib="Adrenal gland tumor"
                                                                                                                                                                                POCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'tissue_type="normal prostate"
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                                                                                                                                                                           lon/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9; Pred. No.
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, Rockville,
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REFERENCE
AUTHORS
TITLE
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g3077057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information. Insert Length: 1144 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA927636 284 bp mRNA EST 10-J om19g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541542 3', mRNA sequence.
      T60003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jnpublished (1997)
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Similarity 100.0%;
9; Conservative
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                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " Job_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/organism="Homo sapiens"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
68 c 64 g
                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib-"Soares_NFL_T_GBC_S1"
/lab_host-"DH10B"
60 c 50 g 76 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1541542"
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284 bp
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Pred. No.
0; Misma
                                                                                                                                                                                                                                                              Score 9; DB 20;
Pred. No. 2.23e+03
0; Mismatches
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2.23e+03;
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                                                                                                                                                                                                                                                                                                                                Length 284;
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      09-FEB-1995
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JOURNAL
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                           126 TTCTCAGAA 134
                                                                                                                                                                                                                                                                          33 ttctcagaa 25
                                                                                                                                                    AA907008 285 bp mRNA EST 09-JUN-1998 ok98c12.s1 NCI_CGAP_LU5 Homo sapiens cDNA clone IMAGE:1522006 similar to gb:M25667 NEUROMODULIN (HUMAN);, mRNA sequence. AA907008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 284)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High gality sequence stops: 212 Source: IMAGE Consortium, LLNL clone is available royalty-free through LLNL; contact the IMAG Consortium (info@image.llnl.gov) for further information. Insert Length: 54 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yc01e11.rl Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:79436 5' similar to gb:x68060 DNA TOPOISOMERASE II, BETA
ISOZYME (HUMAN);contains MER6 repetitive element ;, mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 285)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
                                                                    Homo sapiens
                                                                                     numan.
                                                                                                                       AA907008.1
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                       GI:3042468
                                                                                                                                                                                                                                                                                                                                         Score 9;
Pred. No.
0; Misma
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2.23e+03;
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IMAGE
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LOCUS
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                     Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 292)
Hillier_L., Allen_M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 th
Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3', mRNA sequence.
AA429624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA429624 292 bp mRNA
zw74g10.s1 Soares_test1s_NHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA429624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 87.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Cancer Institute, Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA429624.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1522006"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DHIOB"
a 48 c 96 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Organism="Homo sapiens" pT7T3D-Pac (Pharmacia) with a /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; ist strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "db_xref="taxon.9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:2112725
                                                                                                                    this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this sequence version
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Std Error: 0.00
                        School of Medicine way, Box 8501, St. 1
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. 2.23e+03;
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CDNA clone IMAGE:781986
                             MO 63108
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SOURCE
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                              JOURNAL
MEDLINE
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                  TITLE
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                                                                                                                                                   Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Mai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei; Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
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This clone is available royalty-free through LLNL; contact the Thack Consortium (info@image.llnl.gov) for further information.
                                                          Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria: Primates: Catarrhini: Hominidae: Homo. 1 (bases 1 to 292)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA297030 292 bp mRNA EST 18-APR-1
EST112879 Embryo, 9 week Homo sapiens cDNA 5' end similar
transmembrane protein (GB:U19878, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE Consortium (info@image.llnl.gov) for Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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65 c 77 ;
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1996 this sequence version replaced gi:1294277.
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Pred. No. 2.23e+03
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REFERENCE
AUTHORS
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ACCESSION
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                                                                                                                                              COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERSION
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Best Local S
Matches
                                                                                                                                                                  JOURNAL
MEDLINE
                                                                                                                                                                                                                                            TITLE
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                                                                                                                                                                                                                                                           Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.G., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nugyen, D.T., Pelligrino, S.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nugyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttctcagaa 25
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Seq primer: M13 Reverse.
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Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA344440 292 bp mRNA EST
EST50332 Gall bladder I Homo sapiens cDNA 5'
9712 Medical Center Tel: 3018699056
                                                                                                                                                                                      Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                The Institute for Genomic Research
                                                                    Bioinformatics
                                                                                              Contact: Kerlavage,
                                                                                                                       On Apr 14, 1993 this sequence version Other_ESTs: THC178808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA344440.1 GI:1996679
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Similarity 100.0%;
9; Conservative
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/db_xref="taxon:9606"
/clone_11b="Embryo, 9 week"
/dev_stage="embryo, 9 wks"
45 c 80 g 75 t
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/note="Vector: pBluescript SK-;
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Pred. No.
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                         Rockville, MD 20850 USA
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2.23e+03;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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CE 1 (bases 1 to 293)

RES Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Wirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M. W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fizgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehn, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S., Kelley, J.M., Kilmek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Wedman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Collman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Fischer, C., Husson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Kunsch, C., Ji, H., Li, H., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of CDNA Sequence
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Seq primer: M13 Reverse.
LOCATION OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O6-SEP-1995
EST15394 Human Endothelial cells Homo sapiens cDNA 5' end similar to similar to ribosomal protein L14, mRNA sequence.
T30360
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                           Fax: 3018699423
                                                                                                                                                                                                                                                                                                          Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 2
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_ESTs: THC12476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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/note="Organ: gall bladder; Vector:
Site_1: EcoRi: Site_2: xhoI"
/db_xref="ATCC (inhost):145979"
/db_xref="taxon:9806"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="18 pll.1-gll.2"
/clone_lib="Gall bladder I"
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54 c 49 g 87 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9;
Pred. No.
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2.23e+03;
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                                   243 TTCTGAGAA 251
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 25 ttctgagaa 33
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 294)
Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library
Nature Genet. 4, 373-380 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Sep 12, 1996 this sequence version replaced gi:1393187
Other_ESTs: THC127449
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA369164 294 bp mRNA
EST80533 Placenta II Homo sapiens cDN
containing Alu repeat, mRNA sequence.
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                                                                    h 100.0%;
Similarity 100.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA369164
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                          /organism="Homo sapiens"
/note="organ: placenta; Vector: pE
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):173838"
/db_xref="taxon:9606"
/clone_lib="placenta II"
/tissue_type="placenta"
/dev_stage="fetus"
73 c 70 g 82 t 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="endothelial"
72 c 79 g 69
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/db_xref="taxon:9606"
/clone_lib="Human Endothelial cells"
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                                                                    Score 9;
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                                                                                                                                                                                                                                                                                                         148 TTCTGAGAA 156
                                                                                                                                                                                                                                                              AAOZ/J59 295 bp mRNA EST 16-OCT-1997 nq59e01.s1 NCI_CGAP_CO9 HOMO Sapiens cDNA clone IMAGE:1148184 3 similar to TR:G998901 G998901 PDCD2-PROGRAMMED CELL DEATH-2/RP8 HOMOLOG . ; mRNA sequence.
                                                             g3126551
AA960651.1
                                                                                                                             ub60c01.s1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1382112 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality Seq primer: -40ml3 fwd. ET from Amers High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eutheria: Primates: Catarrhini: Hominidae: Homo.
  Mus musculus
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                                                                                                                                                                            AA960651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
                         house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed by Bento Soares and M. Fatima Bonaldo (Soares 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; ist strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I coligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized, Library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1148184"
/clone_1ib="NCI_CGAP_CO9"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Soares4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 ttctgagaa.33
Complementary DNA sequencing: expressed sequence tags and human genome project science 252, 1651-1656 (1991) 91262645
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 295)
Adams,M.D., Kelley,J.M., Gocayne,J.D., Dubnick,M.,
Polymeropoulos,M.H., Xiao,H., Merril,C.R., Wu,A., Olde,B.,
Moreno,R.F. and etal.
                                                                                                                                                                                                                                                                                                                                                  M62263 295 bp mRNA
EST00332 Hippocampus, Stratagene (cat.
Clone HHCJ48, mRNA sequence.
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
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Similarity 100.0%;
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Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 295)
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/note="Yector: pT7T3D-Pac (Pharmacia) with a modified
/note="Yector: pT7T3D-Pac (Pharmacia) with a modified
/note="Yector: pT7T3D-Pac (Pharmacia) with a modified
/note="Yector a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Ecc RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Ecc RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib-"Soares mouse mammary gland NMLMG"
/sex-"female (lactating)"
/tissue_type-"mammary gland"
/lab_host-"DH10B"
62 c 56 g 89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1382112"
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Pred.
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2.23e+03;
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LOCUS
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Best Local Similarity 100.0%;
Matches 9; Conservative
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1 (bases 1 to 296)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                              Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                               Email: genexpress@genethon.fr
Single read. 18 T removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_idt: alc-18h01
Seq primer: (-21)M13_universal.
                                                                                                                                                                                                                                                                                                                                              Genexpress-Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                            and its expression
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HSC18H012 normalized infant brain cDNA Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
Seg primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive,
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                   Contact: Genethon
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/organisme"Homo sapiens"
/note="Organ: brain; Version: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex-Femmale; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
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/db_xref="ATCC (inhost):37976"
/db_xref="GDB:D0S2472E"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Hippocampus, Stratagene (cat. \#936205)" 62 c 75 g 63 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="HHCJ48"
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                                                                                                                                                          ion/Qualifiers
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Pred. No. 2.23e+03;
0; Mismatches (
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  Query Match 100.0%;
Best Local Similarity 100.0%;
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Best Local (
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172 TTCTCAGAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 180.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rel: (301) 496-1550
Email: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 298)
NCI-CBA http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAI Tumor Gene Index.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:716859
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9; Conservative
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                                                                                                                                                                                                                                                         /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
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Bento Soares, P.N.A.S in press"
                                                                                                                                            /db_xref="taxon:9606"
/map="847A12; 11; 11p15.3-11p15.5"
/clone="IMAGE:1504839"
/clone_lib="Soares_NFL_T_GBC_S1"
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/map="14"
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/dev_stage="3 months old"
58 c 60 g 76
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                                                                                                  /lab_host="DH10B"
50 c 53 ;
                                                                                                                                                                                                                                                    Soares and M. Fatima Bonaldo.
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Pred. No. :
0; Mismat
Score 9;
Pred. No.
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2.23e+03;
  DB 20; Length 298; 2.23e+03;
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SOURCE
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ORIGIN
                                                                         RESULT 145
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JOURNAL
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                   TTCTCAGAA 155
                                    AA363229
EST73119
AA363229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 298)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,Skrizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
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AA161311.1
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                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Differentiated, post mitotic hNT neurons. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'"

/db_xref="gDB:5182041"
                                                    298 bp mRNA
Ovary I Homo sapiens
                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:631961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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1. No. 2.23e+03;
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                                                                                                                                                                                                                                                          Length 298;
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g1746785
                                                                                                                                                                                                                                                                                                                                                                                                                            AA168582 298 bp mRNA EST 12-FEB-1997 ms31h06.r1 Stratagene mouse skin (#937313) Mus musculus cDNA cle IMAGE:608603 5' similar to TR:G1050958 G1050958 CHITOTRIOSIDASE
Contact: Marra M/Mouse EST Project
Washd-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J. Rapid CDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library Nature Genet. 4, 373-380 (1993)
                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Apr 14, 1993 this sequence version replaced gi:692736 Other_ESTs: EST73118 THC167695
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                                                                                          Unpublished (1996)
On Oct 30, 1996 this sequence version
                                                                                                                             The WashU-HHMI Mouse EST Project
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Similarity 100.0%;
9; Conservative
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EcoRI; Site_2: xhoI"
/db_xref="ATCC (inhost):105624"
/db_xref="taxon:9606"
/clone_lib="Ovary I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult, 71
95 c 73 g
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Matches 9; Conservative
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AA977787
                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
On Jan 17, 1998 this sequence version replaced g1:1901028
                                                    Seq
                                                                                                                        Tissue Procurement: L. Jeffrey Medeiros, M.D., Mi
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 299)
                                                                      Insert Length: 489
                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
                                                  primer:
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h quality sequence stop: 278.
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314 286 1810
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                                                                                                                                                                                                                                     Robert_Strausberg@nih.gov
Procurement: L. Jeffrey Medeiros, M.D.,
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                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/1ab_4 c 69 g 77 t
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:608603"
/clone_lib="Stratagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                    -40ml3 fwd. ET from Amersham.
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1. No. 2.23e+03;
Mismatches 0
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IMAGE:1591452
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortlum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Dec 30, 1996 this sequence version replaced gi:1529511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 299)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robert_Strausberg@nih.gov
histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: kidney; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5' GAATTCGGCACGAG 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."
                                                                                                                                                                                  /organism="Homo sapiens"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI;
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected cells.
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/lab_host="SOLR (kanamycin resistant)"
57 c 102 g 63 t
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/map="846F08"
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Pred. No.
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2.23e+03;
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(HUMAN);, mRNJ
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MEDLINE
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Mai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., V.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
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AA336176
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96026280
                                                                                                                                                                                                                                                                                                         Email: arkerlavetigr.org
Email: arkerlavetigr.org
Email: arkerlavetigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human
information related to this EST, please check the TIGR Human
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informatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute for Genomic Research
Medical Center Drive, Rockville,
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/note="Organ: epididymis; Vector: pBluescript SK-; EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):137861"
/db_xref="taxon:9606"
/clone_lib="Epididymus"
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/lab_host="DH10B"
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/clone_1ib="NCI_CGAP_Pr3"
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/db_xref="taxon:9606"
                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                           DEFINITION
                                                                                                                                                       RESULT 151
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Best Local
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Best Local Similarity 100.0%;
                                  ORGANISM
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                                                                                                                                                                                                                                                                                 Match 100.0%;
Local Similarity 100.0%;
les 9; Conservative
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Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                EST.
                                                                                                                         C36182 Yuji Kohara unpu
clone yk455gl 3', mRNA
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Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
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                                                                             g2372323
C36182.1 GI:2372323
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C38297.1 GI:2374534
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Location/Qualifiers
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/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite
tissue_type=whole animal"
/db_xref="taxon:6239"
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/dev_stage="adult"
55 c 66 g
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/clone_lib="Yuji Kohara unpublished cDNA"
/clone_lib="Yuji Kohara unpublished cDNA"
/clone_lib="Yuji Kohara unpublished cDNA"
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Pred. No. 2.23e+03;
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 Mismatches

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LOCUS
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Expression map of the C.elegans genome
Unpublished (1996)
On Sep 21, 1992 this same
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C37813.1
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 300)
Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A.,
Sano, M., Wiyata, A., and Nishigaki, A.
Expression map of the C.elegans genome
Unpublished (1996)
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
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C37813 Yuji Kohara unpu
Clone yk479a6 3', mRNA
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Yata 111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
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Location/Qualifiers
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Location/Qualifiers
                                                 /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/note="dev_stage=waried, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk479a6"
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/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk45591"
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               /clone_lib="Yuji Kohara unpublished cDNA"
75 c 71 g 105 t 2 others
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unpublished cDNA Caenorhabditis
mRNA sequence.
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Best Local Similarity 100.0%;
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                                                                                                                          Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Cukaryota; Metazoa; Nematoda; Secernentea; Rhabditia
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae;
1 (bases 1 to 300)
1 (bases 
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33644 Yuji Kohara unpublished cDNA Caenorhabditis
clone yk374h2 3', mRNA sequence.
C33644
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Artiodactyla; Sulformes; Sulna; Suidae; Sus.
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C95112 Pig back fat Sus
C95112
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C95112.1 GI:3205085
                    Contact: Yuji Kohara
Gene Library Lab
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C33644.1 GI:2365440
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Tel: 81-298-38-2190
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National Institute of Genetics
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Similarity 100.0%;
9; Conservative
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Location/Qualifiers
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Hamasima, N. and Suzuki, H.
                                                                                                     Apr 14, 1993
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/db_xref="taxon:9823"
/clone_lib="pig back fat"
/tissue_type="back fat"
a 62 c 65 g 74 1
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2.23e+03;
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                                                                                                        gi:692546
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
1 (bases 1 to 300)
Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A.,
Sano, M., Miyata, A. and Nishigaki, A.
Expression map of the C.elegans genome
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393967.
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C30237.1 GI:2362033
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Tel: 0559-75-0771
Fax: 0559-75-6240
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Location/Qualifiers
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/strain="CB1489 him-8(e1489)"
/note="dev_stage=waried, sex=Hermaphrodite
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk241a10"
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/strain="CB1489 him-8 (e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
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                                                                                                                              Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 300)

Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A. and Nishigaki,A.

Expression map of the C.elegans genome
Unpublished (1996)
On Sep 12, 1996 this segmence ......
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clone yk472c2 3', mRNA sequence.
C36735
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C32017.1
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Gene Library Lab
Mational: Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderina
1 (bases 1 to 300)
Rohara,Y., Motohashi,T., Tabara,H., Watanabe,H.,
Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
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C32017 Yuji Kohara unpu
Clone Yk314a7 3', mRNA
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
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C32017
                National Institute of Genetics
yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
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C36735.1 GI:2372876
                                                                                     Gene Library Lab
                                                                                                   Contact: Yuji Kohara
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ykohara@ddbj.nig.ac.j.
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Location/Qualifiers
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/strain="CB1489 him-8(e1489)"
/note="dev_stage=waried, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk314a7"
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47 c 58 g &
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RESULT 159
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
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Similarity 100.0%;
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Location/Qualifiers
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/note="dev_stage=varied, sex=Hermaphrodite male,
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/clone="yk472c2"
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/map="889G02; 15; 15q21.3-15q22.2"
/clone="yk415c2"
/clone_11b="yuji Kohara unpublished cDNA"
52 c 65 g 92 t
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/strain="Cal489 him-8 (21489)"
/note="dev_s1489 him-8 (51489)"
tissue_type=whole animal"
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72 c 72 g 104 t 3 others
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
1 (bases 1 to 300)
1 (bases 1, Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigaki, A.
Expression map of the C.elegans genome
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1397760.
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia:
Eukaryota; Ababditoldea; Rhabditidae; Peloderinae; Ca
1 (bases 1 to 300)
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National Institute of Genetics
Yata 1111, Mishina, Shizuoka 411,
Tel: 0559-75-0771
                                                                                                                                                               Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 4
Tel: 0559-75-0771
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Location/Qualifiers
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                                 ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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/note="dev_stage=varied, sex=Hermaphrodite
tissue_type=whole animal"
/db_xref="taxon:6239"
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/clone_lib="Yuji Kohara unpublished cDNA"
      ∕organism="Caenorhabditis elegans"
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Sugimoto, A.,

Caenorhabditis.

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Best Local Similarity 100.0%;
Matches 9; Conservative
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C56383.1
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                           AA382476 300 bp mRNA 5' EST95712 Testis I Homo sapiens cDNA 5'
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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proto-oncogene BMI-1, mRNA sequence
AA382476
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                                                                                                                                                                                                                                                                                                                                      207 TTCTCAGAA 215
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                                                                                                                   US41/8 300 bp mRNA EST 11-SEP-1997 (54178 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk353g7 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.,Jr., Kelley,J.G., Liu,L.-I., Marmaros,S.M., Merley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hadson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Sep 1, 1995 this sequence version replaced Other_ESTs: THC175599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence against 16547 Suppl), 3-174 (1995)
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                      Caenorhabditis elegans
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Similarity 100.0%;
9; Conservative
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Email: arkerlav@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: testis; Vector: p
Ecorl; Site_2: XhoI"
/db_xref-"ATCC (inhost):186783"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
38 c 71 g
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                                                                        GI:2391935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="Testis I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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Pred. No.
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2.23e+03;
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1 (bases 1 to 300)

Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome Unpublished (1996)
On Apr 14, 1993 this sequence version replaced g1:716864.
                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Unpublished (1997)
On Apr 5, 1995 this sequence version replaced gi:
                                     Insert Length: 522 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vata 111, Mishima, Shizuoka 411, Yata 1111, Mishima, Shizuoka 411, Tel: 0559-75-0771
Fax: 0559-75-6240
                                                                                                                                                                                                                                                                    Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nf68h04.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:925111 3',
                                                                                                                                                                                                                                                     M.D., Ph.D
                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                        www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                       cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
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/clone="yk35397"
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70 c 44 g 94 t
Location/Qualifiers
1. .300
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33 ttctcagaa 25
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C53705.1
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Gene Library Lab
Mational Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 300)
Tobaca V Octobach T Tabara H Watanaha H Sudimoto A
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Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
                                                                h 100.0%;
Similarity 100.0%;
9; Conservative
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                             ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/note="Vector: p7773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - Oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p7773 vector. Library went through one round of
normalization. "
/clone="IMACE:925111"
/clone="IMACE:925111"
                                                                                                                                                                                                                        /organism="Caenorhabditis elegans"
/strain="CB189 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite
tissue_type=whole animal"
/db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="colon"
/lab_host="DH10B"
53 c 69 g
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/sex="pooled"
                                                                                                                                                          /clone_lib="Yuji Kohara unpublished cDNA"
38 c 64 g 79 t
                                                                                                                                                                                           /clone="yk323d6"
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                                                                  Score 9;
Pred. No.
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Pred. No.
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C94621.1
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C53842.1
EST.
                                                                                                                                                                                                                                                                                                             C94621 300 bp
C94621 Pig back fat Sus
C94621
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C53842 Xuji Kohara unpu
Clone yk317f5 3', mRNA
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Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:716436.
                                                                                                       On Jan 9, 1998 this sequence version
                                                                                                                       Hamasima, N. and Suzuki, H. Characterization of a porcine fat tissue cDNA library Unpublished (1998)
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Artiodactyla; Sulformes; Sulna; Suldae; Sus. 1 (bases 1 to 300)
                                                                                                                                                                                                                            Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Genetics Yata 1111, Mishima, Shizuoka 411, Tel: 0559-75-0771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yuji Kohara
Gene Library Lab
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
                                     STAFF-Institute
                                                    Animal Genome Research Program Team
                                                                        Contact: Noriyuki Hamasima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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Similarity 100.0%;
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l Ippaizuka, Kamiyokoba, Tsukuba, Ibaraki 305-0854, Japan
81-298-38-2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="871E01; 5; 5q21.3"
/clone="yk317f5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Yuji Kohara unpublished cDNA"
36 c 32 g 103 t
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Pred. No.
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--hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Mai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J.J., Xu, C., Yu, G.L., Ruben, S.M.,
Pillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056 Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Apr 14, 1993 this sequence version replaced gi:785863
Other_ESTs: THC128658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA385118 301 bp mRNA EST 21-APR-1997
EST99723 Thyroid Homo sapiens cDNA 5' end similar to similar to
NADH-UDiquinone oxidoreductase B22 subunit, mRNA sequence.
AA385118
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                          Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96026280
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                         arkerlav@tigr.org
/organism="Homo sapiens"
/note="Organ: thyroid gland; Vector:
Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):189283"
                                                                                                                                      Location/Qualifiers
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/tissue_type="back fat"
44 c 68 g 88
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2.23e+03;
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Mus musculus cDNA clone

16-JUN-1998

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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
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KOZak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
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AA333727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                   Email: arKerlav@tigr.org
Email: arKerlav@tigr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other_ESTs: THC184626
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Apr 14, 1993 this sequence version replaced gi:693230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bioinformatics
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9; Conservative
         91
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/dev_stage="adult"
71 c 82 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/map="9"
/clone_lib="Embryo, 9 week"
/dev_stage="embryo, 9 wks"
73 c 73 g 61 t
                                                                                                 /map="1
                                                                                                                                  /db_xref="ATCC (inhost):135392"
/db_xref="taxon:9606"
                                                                                                                                                                                                                          note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                              ∕organism="Homo sapiens"
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mRNA sequence.
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COMMENT
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AUTHORS
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SOURCE
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                                                                                                           BASE COUNT
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Best Local Similarity 100.0%;
Matches 9; Conservative
             Query Match
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1 (bases 1 to 301)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
Unpublished (1996)

On Jan 17, 1998 this sequence version replaced gi:2044829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI019762 301 bp mRNA EST uas00904.r1 Soares mouse mammary gland NbMMG IMAGE:1364790 5', mRNA sequence.
AI019762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector to vector length is 302
Seg primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the LANGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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AI019762.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                    T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                     /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/8 c 58 g 111 t
                                                                                                                                                                                                                                                                     /clone_lib="Soares mouse mammary
                                                                                                                                                                                                                                                                                        /clone="IMAGE:1364790"
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/map="Chromosome 11"
                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:3234098
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             Score 9;
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No. 2.23e+03
                DB 21;
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Louis,

MO 63108

contact the

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SOURCE

AUTHORS

VERSION KEYWORDS

NID ACCESSION B

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BASE COUNT
ORIGIN
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LOCUS
                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RS Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White, O., Sutton, G., Blake, J. A., Brandon, R. C., Man-Mai, C., Clayton, R. A., Cline, T. R., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzperald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E. Hinkle, P. S. Jr., Kelley, J. M., Kelley, J. C., Liu, L. T., Marmaros, S. M., Merrick, J. M., Moreno-Palanques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Moreno-Palanques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, D. -F., Ferrie, A., Fischer, C., Hastings, G. A., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Kozak, D. L., Kunsch, C., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M. and Venter, J. C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA381889 302 bp mRNA EST · 21-APR-1997 EST95202 Activated T-cells I Homo sapiens cDNA 5' end, mRNA
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On Sep 12, 1996 this sequence version replaced gi:1407216.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 302)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Other_ESTs: THC168705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 3018699423
                                                                                                                                                                                       /clone_lib="Activated T-cells I"
/cell_type="T-lymphocyte"
/dev_stage="adult"
                                                                                                                                                                                                                                                             /db_xref="ATCC (inhost):186435"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                      'note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                               Score 9;
Pred. No.
0; Misma
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M1smatches 0;
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sequence.
AA712997
g2722914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 299.
Location/Qualifiers
                                                                      AA712997 302 bp mRNA EST 32557 Lambda-PRL2 Arabidopsis thaliana cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA626881 302 bp mRNA EST 15-OCT-1997 2089h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745223 3', mRNA sequence.

AA626881
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On Sep 12, 1996 this sequence version replaced gi:1288460.
                                                                                                                                                                                                                                                                                      h 100.0%;
Similarity 100.0%;
9; Conservative
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Eutheria;
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theria; Primates;
(bases 1 to 302)
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
Adb_xref="GDB:593033"
                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH108"
45 c 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:745223"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
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Pred. No. 2.23e-
0; Mismatches
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2.23e+03;
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220L22T7, mRNA
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TITLE

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33 ttctcagaa 25
                                                                                                                                                                                            g514725
T14558.1
                                               Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 304)
Franco,G.R., Adams,M.D., Soares,M.B., Simpson,A.J.G., Venter,J.C.
                                                                                                                                                                                                                                   SMEST0219 Schistosoma mansoni,
Schistosoma mansoni cDNA clone
T14558
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On Sep 1:
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EST.
                                                                                                                                                                                                                                                                                                 T14558
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Seq primer: T7 dye primer.
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Tel: 517-353-0854
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1 (bases 1 to 302)
Identification of new Schistosoma mansoni genes by the EST strategy using a directional cDNA library
                                    and Pena, S.D.J.
                                                                                                                                                       Schistosoma mansoni.
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MSU-DOE Plant Research Laboratory
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligo dT primed cDNA.
/db_xref="taxon:3702"
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53 c 73 g 7
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/clone="220I
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/strain="var columbia"
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2.23e+03;
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SMPAI59 3' end, mRNA sequence.
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                                                             Tumor Gene Index
Unpublished (1997)
On Apr 14, 1993 th
                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Chominidae; Homo.

1 (Dases 1 to 304)

1 (Dases 1 to 304)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
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95137379
Contact: Robert Strausberg, Ph.D.
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Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 100.0%;
Similarity 100.0%;
9; Conservative
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Fax: (5531)4415409
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primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Schistosoma mansoni,
Franco"
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56 c 55 g 9
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/strain="NMRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:317940
                                                             this sequence version replaced g1:503472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9;
Pred. No.
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CDNA clone IMAGE:1620069
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                                                                                                                                                                          Project (CGAP),
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RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.G., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Knnsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA313179 305 bp mRNA EST 19-APR-195
EST18492 Liver, subtracted (abundant clones) I Homo sapiens
end similar to similar to albumin, mRNA sequence.
AA313179
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 305)
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EST.
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High quality sequence stop: 292.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: M. Bento Soares, Ph.D.,
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Email: Robert_Strau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 657
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/organism="Homo sapiens"
/note="vector: pT733D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cD
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
51 c 51
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No. 2.23e+03
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Best Local
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96026280
                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA760552 305 bp mRNA EST 23-JAN-15 vv78e11.r1 Stratagene mouse skin (#937313) Mus musculus cDh IMAGE:1228556 5' similar to gb:X68836 S-ADENOSYLMETHIONINE SYNTHETASE GAMMA FORM (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                     Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 305)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa;
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Seq primer: M13 Reverse.
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Apr 14, 1993 this sequence version replaced gi:692643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser, C.M. and Venter, J.C.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA760552.1 GI:2808346
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
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EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):117113"
/db_xref="taxon:9606"
/map="22; 804C11; 5; 5923.3-5931.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Liver, subtracted (abundant clones)
/dev_stage="adult"
57 c 68 g 71 t
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2.23e+03;
                                                                                                                                                                                                         replaced gi:1405065
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                        Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Welnstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchnan, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W. W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G. L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 8 million nucleotides of cDNA sequence
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 3018699056
                                                                                                         96026280
On Apr 14, 1993 this sequence version replaced g1:692610.
Other_ESTs: THC172063_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA313174 306 bp mRNA EST18461 Liver, subtracted (abundant c end similar to albumin, mRNA sequence. AA313174
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High quality sequence stop: 296.
Location/Qualifiers
                                                                                                    Contact: Kerlavage, AR
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 306)
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/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
57 c 77 g 95 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 9;
Pred. No.
0; Misma
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1. No. 2.23e+03;
Mismatches 0;
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                             MD 20850 USA
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Best Local Similarity 100.0%;
Matches 9; Conservative
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25 ttctgagaa 33
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Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 306)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 297.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
On Jan 9, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA881995.1
                                                                                                                                                                                                                             MGI:668858
                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                               Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                               mouseest@watson.wustl.edu
/note-*Organ: liver; Vector: pBluescript SK-;
EcoRI; Site_2: KhoI"
/db_xref-*NATCC (Inhost):117087"
/db_xref-*taxon:9906"
/map-*972H07; 12; 12q15-q21.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Liver, subtracted
/dev_stage="adult"
    63 c    74 g    69 t
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Pred. No.
0; Misma
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. 2.23e+03;
---hes 0;
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musculus cDNA clo
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Query Match 100.0%;
Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                   Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex,
Tel: 33169472800
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1 (bases 1 to 306)

Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
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F11767.1 GI:706075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F11767 306 bp mRNJ
HSC31C111 normalized infant
C-31C11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genexpress-Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Genethon
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R. Acad. Sci. III,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genexpress@genethon.fr
                                                                                                                                                                       /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NoLI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5′-> 3′ into the HindIII -> NotI sites of the lafmid BA vector. Clone 11brary from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="lung"
/dev_stage="6-8 month old"
/lab_host="SOLR (kanamycin resistant)"
/lab_nost="SOLR (kanamycin resistant)"
                                                                     /tissue_type="total brain"
/dev_stage="3 months old"
63 c 75 g 71 t
                                                                                                                          /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
                                                                                                                                        /clone_lib="normalized infant
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Stratagene mouse
                                                                                                                                                            /clone="c-31c11"
   Score
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   DB 19; Length 306; 2.23e+03;
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95277534
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L25482.1
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 308)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
                                                                                                                                                                                                                                           F07471 308 bp mRN7
HSC27A041 normalized infant
c-27a04, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Human Genome Center
Lawrence Berkeley Laboratory
1 Cyclotron Road, Berkeley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 308)
Cheng, J.-F. F., Zhu, Y. and Boyartchuk, V.L. Isolation and mapping of human chromosome a chromosome 21 expression map Genomics 23, 75-84 (1994)
                                       and
                                                 Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                          EST
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Eutheria; Primates;
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21, 1992 this
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/mar="01"
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96 c 92 g
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HL 1065a Homo sapiens
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Catarrhini; Hominidae;
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0; M
sequence version replaced gi:276446
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FEATURES

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Email: est@watson.wustl.edu
Insert Size: 693
Insert Size: 693
High quality sequence stops: 282 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9718592
T90079.1
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T90079
                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T90079 308 bp mRNA EST 20-MAR-1995 yd39b06.sl Soares fetal liver spleen lNFLS Homo sapiens cDNA clonimaGE:110579 3' similar to gb:M31303_rnal STATHMIN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarriini; Hominidae; Homo.

1 (bases 1 to 308)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba; T., E.,W., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T. L., Soares,M., Tan,F., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rohlfing,T., Rohlfing
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
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/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5′ -> 3′ into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
/db_xref="taxon:9606"
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/dev_stage="3 months old"
68 c 79 g 80 t
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/clone_lib="normalized infant brain cDNA"
/sex="Female"
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                                                                                                                                                               Tel: 314 286 1800

Fmax: 314 286 1810

Email: est@watson.wustl.edu

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 255.

Location/Qualifiers
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AA419174
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1 (bases 1 to 309)

Hillier_L. Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 693 Std Error:
Seq primer: -21m13
High quality sequence stop: 282.
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AA419174.1
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Similarity 100.0%;
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/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco:RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
[5' ARCTGGAAGAATTAAAGAACTTTTTTTTTTTTTTTTTTT']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
/db_xref="sobs:466196"
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                                               /Organism="Homo sapiens"
/note="Organ: ovary: Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
/lab_host="DH10B (ampicillin resistant)"
77 c 66 g 114 t 1 other
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/clone="IMAGE:110579"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE Consortium (info@image.llnl.gov) for Insert Length: 589 Std Error: 0.00 Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S. Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST project 1997
Unpublished (1997)
On Dec 30, 1996 this sequence version replaced gi:1529016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 310)
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                                                                                                                     /organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbH11W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260332-265223,
340488-34579, and 484488-489479."
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/db_xref="taxon:9606"
/clone="IMAGE:755576"
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the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
98 c 89 g 60 t
/clone_lib~"Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                     /db_xref="taxon:9606"
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                                                 clone="IMAGE:682122"
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 930

High quality sequence stops: 281 Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.lhnl.gov) for further information.

Insert Length: 930 Std Error: 0.00
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1 (bases 1 to 310)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T88794 310 bp mRNA EST yd32a08.s1 Soares fetal liver spleen lNFLS IMAGE:109910 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 281.
Location/Qualifiers
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T88794.1 GI:717307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson, R.
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Similarity 100.0%;
9; Conservative
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                                                                                                                                                                                  /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
54 c 67 g 114 t 1 others
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60 c 65
                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:109910"
                                                                                                                                         /clone_lib="Soares
                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                            /sex="male"
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2.23e+03;
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AA146289 311 bp
mr06g07.r1 Soares mouse
5', mRNA sequence.
AA146289
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 310)
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AA502331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ellas Campo, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www-bio.llnl.gov/bbrp/image/image.html
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cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NA502321.1 GI:2237288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
polylinker; Site_1: Not I = Site_2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I = oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library went through one round of
normalization. "Cor"
                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Co3"
/sex="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:898522"
                                                                                                                                                                                                                                                                                                                                                  /tissue_type="colon"
/lab_host="DH10B"
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Pred. No. :
0; Mismai
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                                        3NbMS Mus musculus cDNA clone IMAGE:596700
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o. 2.23e+03;
---hes 0;
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AA146289.1
EST.
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                                                                g614109
T32011.1
                                                                                                 to gastrin-binding T32011
                                                                                                               T32011 312 bp mRNA EST 06-SEP-1995 EST42478 Human Uterus Homo sapiens cDNA 5' end similar to sim to gastrin-binding protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project Unpublished (1996)
Homo sapiens
Eukaryota; M
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Location/Qualifiers
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Similarity 100.0%;
9; Conservative
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
a 48 c 52 g
                                                                    GI:614109
                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10000"
/clone="IMAGE:596700"
/clone_lib="Soares mouse 3NbMS"
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Pred. No. 2.23e+03;
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Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   AA724581 312 bp mRNA EST 31-D; ai01b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327293 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd. Gaithersburg, MD 2
                                                                       Tumor Gene Index Unpublished (1997)
                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 312)
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                                                                                                                                                                                                                                                                                                                            AA724581.1
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                                               18, 1996 this sequence version replaced gi:1366624.
Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Homo sapiens"
/note-"Organ: uterus"
/db_xref-"ATCC (inhost):102354"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Human Uterus"
75 c 71 g 86
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Pred. No.
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2.23e+03;
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. (
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA713645 313 bp
nv80h11.s1 NCI_CGAP_Br4
            CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                On Sep 12, 1996 this sequence version replaced gi:1404722
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 313)
www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Similarity 100.0%;
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/lab_host="DH10B"
65 c 44 g 134 t
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIO06978 315 bp mRNA EST 12-JUN-1998 ua77f02.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1363515 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
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h quality sequence stop: 292.
Location/Qualifiers
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/note-"Organ: breast: Vector: pAMP10; mRNA made from normal breast ductal tissue, Chan made by oligo-dr priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383." /db_xref="taxon:9606" /clone="IMAGE:1236165" /clone="image:12361656] /clone="image:12361656] /clone="image:123616566] /clone="ima
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/lab_host="DH10B"
60 c 59 g 112 t
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0; Mismatches (
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LOCUS
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25 ttctgagaa 33
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AA508995 315 bp mRNA
MBAFCX6A07T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia
malayi cDNA clone AFCX6A07 5', mRNA sequence.
AA508995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mark.blaxter@ed.ac.uk
The ABI trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/AFC/MBAFCX6A07T3.html
full sequence of the cDNA clone. The polyA tail has
and is excluded from this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3JT, UK.
Tel: +44 131 650 6760
Fax: +44 131 670 5450
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Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes expressed in adult female Brugia malayi
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brugia malayi
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blaxter, M.L., Waterfall, M., Daub, J., Lizotte, M.,
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Similarity 100.0%;
9; Conservative
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1 (bases 1 to 315)
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                                                                                                                          /Organism="Brugia malayi"
//organism="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
//orde="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
//orde="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Lymphatic filarial nematode parasite of humans.

MRNA was prepared from approximately 50 adult females
isolated from the peritoneal cavity of jirds and
isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 5 x 10E6 independent recombinants
and the average insert size is -900bp.The library was
constructed by
Michelle Lizotte-Wanlewski. The
''harvy is available from Dr.S.A.Williams, email:
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/dev_stage="4 weeks"
/lab_host="DH10B"
a 55 c 59 g
                                                                        genome@smith.edu."
/db_xref="taxon:6279"
/clone="AFCX6A07"
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/db_xref="taxon:10090"
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l. .315
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                      /clone_lib="Brugia malayi adult female cDNA
(SAW96MLW-BmAF)"
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/sex="female"
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Pred. No. 2.23e
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). 2.23e+03;
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                                          / Match 100.0%;
Local Similarity 100.0%;
nes 9; Conservative
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                      TTCTGAGAA 146
                                                                                                                                                                                                                                                                                                                                                                                           rel: (301) 496-1550
Email: Robert 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
AA252619 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ52619 316 bp mRNA EST 13-AUG-1997 25144006.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685163
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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Similarity 100.0%;
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                                                                                                                                                        /clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center
/lab_host="DH10B"
88 c 90 g 53 t
                                                                                                                                       /clone="IMAGE:685163"
                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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AA230352
                                                                                                                                                         T12492 317 bp n
B079R Heart Homo sapiens
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       100.0%;
Similarity 100.0%;
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Eutheria; F
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                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: kidney; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: xhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP xR Vector; -5' adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3' Library provided by Lisa Guay-Woodford."
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib-"GuayWoodford Beier mouse kidney day
/tissue_type-"kidney"
/dev_stage="juvenile (7 days old)"
/lab_host="SOLR (kanamycin resistant)"
47 c 46 g 106 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                       Score 9;
Pred. No.
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Tel: 091 44 23
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KJ4SLBY5D4SL JHU93SL-BmL4 (JHU) Brugia malayi cDNA clone
clone Y5D4 5' end, mRNA sequence.
                                                                                                                                                                       Seq
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Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                            Sabarinathan, R., Kannan, K., Rao, K.V.N., Ravi, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brugia malayi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Banting Institute, 100 College St., Toronto, Ontario, M5G1L5 Tel: 4169788758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_ESTs: B079F
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Liew, C.C., Hwang, D.M., Fung, Y.W., Laurenssen, C., Cukerman, E.,
                                                                                                                                                                                                                                                         Anna University
                                                                                                                                                                                                                                                                            Centre for Biotechnology
                                                                                                                                                                                                                                                                                            Contact: Kunthala Jayaraman
                                                                                                                                                                                                                                                                                                                                                                              Jayaraman,K.
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Similarity 100.0%;
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/organism="Brugia malayi"
/note="Vector: Uni-ZAP XR; Site_1: Xba I; Site_2: EcoR I;
/note="Vector: Uni-ZAP XR; Site_1: Xba I; Site_2: EcoR I;
The cDNA library of the B.malayi L4 stage was constructed at Johns Hopkins University. The presence of a conserved 2 nucleotide splice leader at 5'end of large proportion of mature messages was exploited in the linked Reverse transcriptase-polymerase chain reaction in the construction of this library. The library had unamplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/note="Vector: Lambda gtll;
/db_xref="taxon:9606"
/clone="B079"
                                                                                                                                                                                                                                                                                                                            1997 this sequence version replaced gi:931942
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85 c 86 g 6
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Pred. No. 2.23e+03;
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 317)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,; Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashD.NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3', mRNA sequence.
AA626165
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zu90b10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745243
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Fax: 314 286 1810
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Acknowledgements: Nithyakalyani Raghavan, Inca Ghosh, Ward Eisinger, Alan Scott Dept. of Molecular Microbiology and Immunology School of Public health and Hygiene, Johns Hopkins University, 615, N.Wolfe street, Baltimore MD 21205, USA, Tel 410 955 3442 Fax: 410 955 0105 "/clone="B.malayi clone Y5D4"/clone="B.malayi clone Y5D4"/clone=11b="My039XL-BmL4"/clone_11b="My039XL-BmL4"/clone_11b="My039XL-BmL4"/clone_11b="My039XL-BmL4"/clone_11b="My039XL-BmL4"/lab_host="XL-1 Blue MKF'"
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                                                                                                                                                 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "db_xref="GDB.5933120"
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/organism="Homo sapiens"
/note="Vector: pT7T3D-read (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDI
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDI
was prepared from mRNA obtained from Clontech
was prepared from mRNA obtained with a Not I - oligo(dT)
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:745243"
/sex="male"
/lab_host="DH10B"
                                                                /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Pred. No. 2.23e+03;
0; Mismatches 0
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further information.
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Best Local Similarity 100.0%;
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Et theria; Primates; Catarrhini; Hominidae; Homo.

Et 1 (bases 1 to 319)

Et 1 (bases 1 to 319)

Et 1 (bases 1 to 319)

Et 2 (bases 1 to 319)

Et 3 (bases 1 to 319)

Et 3 (bases 1 to 319)

Et 4 (bases 1 to 319)

Et 4 (bases 1 to 319)

Et 5 (bases 1 to 319)

Et 6 (bases 1 to 319)

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Et 7 (bases 1 to 319)

Et 7 (bases 1 to 319)

Et 7 (bases 1 to 319)

Et 8 (bases 1 to 319)

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96026280
On Sep 1:
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AA301326
                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Drive, Rockvill Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
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                                                                                                                                                               /organism="Homo sapiens"
/note="Organ: testis; Vector: pl
EcoRI; Site_2: XhoI"
/db_xref="ARCC (inhost):191679"
/db_xref="taxon:9606"
                                                                                                                /clone_lib="Testis tumor"
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vt30h07.r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2153564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 319)
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Location/Qualifiers
                                                                                                                                                              107
                                                                                                                                                                                                                                                                        /clone_lib-"Barstead mouse proximal colon MPLRB6"
/dev_stage-"7 day juvenile"
/lab_host-"DH10B"
79 c 57 g 76 t
                                                                                                                                                                                                                                                  [AATTCGGATCCTTG], digested with Not Not I and Eco RI sites of the modif Library constructed by Bob Barstead./db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                 clone="IMAGE:1164637"
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Pred. No.
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Search completed: Thu Oct 28 00:29:41 1999

Job time : 228 secs.